



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 162063

TO: Sumesh Kaushal
Location: 2B85/2C70
Art Unit: 1633
Friday, August 19, 2005

Case Serial Number: 10/617835

From: Deirdre Arnold
Location: Biotech-Chem Library
REM 1A64
Phone: 571-272-2532

Deirdre.Arnold@uspto.gov

Search Notes

Please feel free to contact me if you have any questions or would like to amend the search.

Thank you for using STIC services.

Regards,
Deirdre Arnold



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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 18, 2005, 21:01:19 ; Search time 126 Seconds
(without alignments)
982.249 Million cell updates/sec

Title: US-10-617-835-4

Perfect score: 1645

Sequence: 1 MRARLLIFLPSVFILSAAG.....SHEGYSDEAVRHRGQGP 320

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq.15dec04:*
1: _geneseq.1980s:*
2: _geneseq.1990s:*
3: _geneseq.2000s:*
4: _geneseq.2001s:*
5: _geneseq.2002s:*
6: _geneseq.2003as:*
7: _geneseq.2003bs:*
8: _geneseq.2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1645	100.0	320	AAW18785	AAW18785 Neisseria
2	1641	99.8	320	AAW38540	AAW38540 Neisseria
3	1641	99.8	320	AAW75812	AAW75812 Neisseria
4	1641	99.8	320	AAW74926	AAW74926 Neisseria
5	1641	99.8	320	AAW58587	AAW58587 N. gonorr
6	1641	99.8	320	AAW58587	AAW58587 N. gonorr
7	1641	99.8	320	ABP76947	ABP76947 N. gonorr
8	1634	99.3	320	AAW38538	AAW38538 Neisseria
9	1634	99.3	320	AAW74927	AAW74927 Neisseria
10	1634	99.3	320	AAW75811	AAW75811 Neisseria
11	1634	99.3	320	AAW58586	AAW58586 N. mening
12	1634	99.3	320	AAW58586	AAW58586 N. mening
13	1634	99.3	320	AAW38539	AAW38539 Neisseria
14	1624	98.7	320	AAW74928	AAW74928 Neisseria
15	1624	98.7	320	AAW75813	AAW75813 Neisseria
16	1624	98.7	320	AAW58588	AAW58588 N. mening
17	1624	98.7	320	AAW58588	AAW58588 N. mening
18	1624	98.7	320	ABP79829	ABP79829 N. gonorr
19	1602	63.3	213	AAW38537	AAW38537 N. mening
20	1030	62.6	313	AAW38537	AAW38537 Neisseria
21	1030	62.6	313	ABP78726	ABP78726 N. gonorr
22	1030	62.6	313	ABP80805	ABP80805 N. gonorr
23	1025.5	62.3	314	AAW38655	AAW38655 Neisseria
24	1022	62.1	313	AAW38656	AAW38656 Neisseria
25	650	39.5	197	AAW38654	AAW38654 Neisseria

26	117.5	7.1	1250	4	ABW5508
27	117.5	7.1	1250	4	ABW5508
28	106.5	6.5	190	7	ADP04155
29	106.5	6.5	506	7	ABW66253
30	102.5	6.2	1250	3	AAW59361
31	101	6.1	445	6	ABU24747
32	100.5	6.1	1499	4	ABW58409
33	99.5	6.0	756	5	ABW58409
34	99	6.0	872	6	ABU27543
35	97	5.9	515	7	ABW64118
36	96.5	5.9	685	7	AAU76449
37	96	5.8	274	8	ADQ58765
38	96	5.8	274	8	ADQ58765
39	96	5.8	684	3	AAW59318
40	96	5.8	729	4	ABG29804
41	95	5.8	274	8	ADQ58761
42	95	5.8	274	8	ADQ58763
43	95	5.8	274	8	ADQ58766
44	95	5.8	424	6	ADQ58766
45	94.5	5.7	343	2	AAW00088

ALIGNMENTS

RESULT 1	AAW18785	standard; protein, 320 AA.
ID	AAW18785	
XX	AAW18785;	
AC	10-DEC-1997	(first entry)
DT	10-DEC-1997	(first entry)
DE	Neisseria adhesion protein (from Orf1).	
XX	Neisseria gonorrhoeae; adhesion; lipoprotein; OrfA; OrfI; OrfB.	
KW	Neisseria gonorrhoeae.	
XX	Neisseria gonorrhoeae.	
OS	Neisseria gonorrhoeae.	
PN	DE19534579-A1.	
PD	20-MAR-1997.	
XX	18-SEP-1995;	95DE-01034579.
PF	18-SEP-1995;	95DE-01034579.
XX	18-SEP-1995;	95DE-01034579.
PR	18-SEP-1995;	95DE-01034579.
XX	(PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.	
PA	WPI; 1997-180942/17.	
DR	WPI; 1997-180942/17.	
XX	Nucleic acids encoding Neisseria adhesion proteins - for therapeutic and diagnostic use.	
PT	diagnostic use.	
XX	Claim 29; Page 11-13; 20pp; German.	
PS	OrfA and OrfB in complexes with the protein plic are capable of adhering to human cells. Products obtained from the DNA are useful in medicaments, CC diagnostic compans. and vaccines, esp. for treatment of Neisseria CC gonorrhoea and N. meningitidis infections	
XX	Sequence 320 AA;	
SO	Query Match	100.0%; Score 1645; DB 2; Length 320;
	Best Local Similarity	100.0%; Pred. No. 1.2e-151;
	Matches	320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy	1 MRARLLIFLPSVFILSAAGTLTGPISHGGGRFAVEQELVAASRAAVKMDLQALHGR 60	
Db	1 MRARLLIFLPSVFILSAAGTLTGPISHGGGRFAVEQELVAASRAAVKMDLQALHGR 60	
Qy	61 KVALYATMGDSGSLTGRYSIDALIRGEYINSPAVRTDYTPYRTAETTSGLTG 120	

DB 61 KVALIATMDQSGSLTGRYSIDALIRGEYINSPAVRTDYYPRYETTAETTSGGITG 120
QY 121 LTTSLSTLNAPALSRTOGSGSRSSLGINIGMGVDYRNETLTTPRPTAFLSHVGVVF 180
DB 121 LTTSLSTLNAPALSRTOGSGSRSSLGINIGMGVDYRNETLTTPRPTAFLSHVGVVF 180
QY 181 FLRGIDVVSPPANADTDVFINIDVFCTIRNRTEMHLYNAETLKAQTKLEYFAVDRTNNKLL 240
DB 181 FLRGIDVVSPPANADTDVFINIDVFCTIRNRTEMHLYNAETLKAQTKLEYFAVDRTNNKLL 240
QY 241 IKPRTNAFEAAKYKENYALMGPYKVSKGIKPTEGLMVDPSDIRPYGNHTGNSAPSV EADN 300
DB 241 IKPRTNAFEAAKYKENYALMGPYKVSKGIKPTEGLMVDPSDIRPYGNHTGNSAPSV EADN 300
QY 301 SHEGYGYSDEAVRQHRQGP 320
DB 301 SHEGYGYSDEAVRQHRQGP 320

RESULT 2
AA38540
ID AA38540 standard; protein; 320 AA.
XX
AC AAY38540;
XX
DT 08-OCT-1999 (first entry)
XX
DE Neisseria gonorrhoeae antigenic protein encoded by ORF15.
XX
KM Neisseria meningitidis; Neisseria gonorrhoeae; antigen; vaccine;
KM treatment; Neisseria infection; meningitis; septicemia; gonorrhea.
XX
OS Neisseria gonorrhoeae.
XX
PN WO9924578-A2.
XX
PD 20-MAY-1999.
XX
PF 09-OCT-1998; 98WO-1B001665.
XX
PR 06-NOV-1997; 97GB-00023516.
PR 14-NOV-1997; 97GB-00024130.
PR 18-NOV-1997; 97GB-00024386.
PR 27-NOV-1997; 97GB-00025158.
PR 10-DEC-1997; 97GB-00026147.
PR 14-JAN-1998; 98GB-00000759.
PR 01-SEP-1998; 98GB-00019016.
XX
PA (CHIR-) CHIRON SPA.
XX
PI Masignani V, Rappuoli R, Pizza M, Scarlato V, Grandi G;
XX
XX WPI: 1999-327407/27.
DR N-PSDB; AA212008.
XX
PT Proteins from Neisseria meningitidis and N. gonorrhoeae useful for
PT diagnosis, treatment and prevention of infection.
XX
PS Claim 4; Page 100; 524pp; English.
XX
CC Amino acid sequences AAY38499-Y38944 represent Neisseria meningitidis and
CC N. gonorrhoeae antigenic proteins. They are encoded by open reading
CC frames (ORFs) AA211972-212358. The antigenic proteins, their fragments,
CC their nucleic acids and antibodies are used for diagnosis, prevention (as
CC vaccines) or treatment of Neisseria infections, such as meningitis,
CC septicemia and gonorrhea. Both organisms are closely related. Fragments
CC of the nucleic acids are useful as hybridisation probes and antisense
CC reagents
XX
SQ Sequence 320 AA;

Query Match 99.8%; Score 1641; DB 2; Length 320;
Best Local Similarity 99.7%; Pred. No. 2.8e-151;

Matches 319; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 MRARLLPILESVLTILSACGTLTGIPSHGGKRFABEOLVVASARAAVKMDLQALHGR 60
DB 1 MRARLLPILESVLTILSACGTLTGIPSHGGKRFABEOLVVASARAAVKMDLQALHGR 60
QY 61 KVALIATMDQSGSLTGRYSIDALIRGEYINSPAVRTDYYPRYETTAETTSGGITG 120
DB 61 KVALIATMDQSGSLTGRYSIDALIRGEYINSPAVRTDYYPRYETTAETTSGGITG 120
QY 121 LTTSLSTLNAPALSRTOGSGSRSSLGINIGMGVDYRNETLTTPRPTAFLSHVGVVF 180
DB 121 LTTSLSTLNAPALSRTOGSGSRSSLGINIGMGVDYRNETLTTPRPTAFLSHVGVVF 180
QY 181 FLRGIDVVSPPANADTDVFINIDVFCTIRNRTEMHLYNAETLKAQTKLEYFAVDRTNNKLL 240
DB 181 FLRGIDVVSPPANADTDVFINIDVFCTIRNRTEMHLYNAETLKAQTKLEYFAVDRTNNKLL 240
QY 241 IKPRTNAFEAAKYKENYALMGPYKVSKGIKPTEGLMVDPSDIRPYGNHTGNSAPSV EADN 300
DB 241 IKPRTNAFEAAKYKENYALMGPYKVSKGIKPTEGLMVDPSDIRPYGNHTGNSAPSV EADN 300
QY 301 SHEGYGYSDEAVRQHRQGP 320
DB 301 SHEGYGYSDEAVRQHRQGP 320

RESULT 3
AA75812
ID AA75812 standard; protein; 320 AA.
XX
AC AAY75812;
XX
DT 12-SEP-2003 (revised)
DT 21-MAR-2000 (first entry)
XX
DE Neisseria gonorrhoeae ORF 406 protein sequence SEQ ID NO.3112.
XX
KM Neisseria meningitidis; Neisseria gonorrhoeae; antigen; vaccine;
KM antigenic; diagnosis; immunogenic; infection; meningitis; septicemia;
KM antibacterial; gene therapy.
XX
OS Neisseria gonorrhoeae.
XX
PN WO9957280-A2.
XX
PD 11-NOV-1999.
XX
PF 30-APR-1999; 99WO-US009346.
XX
PR 01-MAY-1998; 98US-0083758P.
PR 31-JUL-1998; 98US-0094869P.
PR 02-SEP-1998; 98US-0098994P.
PR 02-SEP-1998; 98US-0099062P.
PR 09-OCT-1998; 98US-0103749P.
PR 09-OCT-1998; 98US-0103794P.
PR 09-OCT-1998; 98US-0103796P.
PR 25-FEB-1999; 99US-0121528P.
XX
PA (CHIR-) CHIRON CORP.
PA (GENO-) INST GENOMIC RES.
XX
PI Fraser C, Galeotti C, Grandi G, Hickey E, Masignani V, Mora M,
PI Petersen J, Pizza M, Rappuoli R, Ratti G, Scarlato V, Scarselli M;
PI Tettelin H, Venter JC;
XX
XX WPI: 2000-062150/05.
DR N-PSDB; AA254614.
XX
PT Novel Neisserial polypeptides predicted to be useful antigens for
PT vaccines and diagnostics.
PS Example 1; Page 109; 1453pp; English.

XX AA253015 to AA254536, AA254577 to AA254615, and AA274253 to AA275941
 CC represent novel *Neisseria meningitidis* and *N. gonorrhoeae* polynucleotides
 CC and polypeptides. AA254537 to AA254576 and AA254616 to AA254617 represent
 CC PCR primers used in the exemplification of the present invention. The
 CC polypeptides, the polynucleotides, antibodies and compositions of the
 CC invention can be used as vaccines, as diagnostic reagents, and as
 CC immunogenic compositions. The polypeptides can be used in the manufacture
 CC of medicaments for treating or preventing infection due to *Neisseria*
 CC bacteria (e.g. meningitis and septicemia), to detect the presence of
 CC *Neisseria* bacteria, or to raise antibodies. They may also be used to
 CC screen for agonists or antagonists, which may themselves have use as
 CC antibacterial agents. The polynucleotides of the invention may also be
 CC used in gene therapy protocols. (Updated on 12-SEP-2003 to standardise OS
 CC field)

XX Sequence 320 AA;
 SQ

Query Match 99.8%; Score 1641; DB 3; Length 320;
 Best Local Similarity 99.7%; Pred. No. 2.8e-151;
 Matches 319; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRARLLIPILPSVFLISACGTLTGIPSHGGKRRFAVEQELVAASRAAOKMDLQALHGR 60
 DB 1 MRARLLIPILPSVFLISACGTLTGIPSHGGKRRFAVEQELVAASRAAOKMDLQALHGR 60
 QY 61 KVALYIATMGDQSGSLTGRYSIDALIRGEYINSPAVRTDVTYPRYETTAETTSGLTG 120
 DB 61 KVALYIATMGDQSGSLTGRYSIDALIRGEYINSPAVRTDVTYPRYETTAETTSGLTG 120
 QY 121 LTTSLSTINAPALSTGDSGSRSLGNTGMDYNNETLTNPRDTAFSLHVQTVF 180
 DB 121 LTTSLSTINAPALSTGDSGSRSLGNTGMDYNNETLTNPRDTAFSLHVQTVF 180
 QY 181 FLRGIDVVS PANADTVFINIDVFGTIRNRTEMLYNAETLKAQTKLEFPAVDRTNKKLL 240
 DB 181 FLRGIDVVS PANADTVFINIDVFGTIRNRTEMLYNAETLKAQTKLEFPAVDRTNKKLL 240
 QY 241 IKPKNNAEFAAYKENYALMMPYKVKIKPTGEGLVMPDSDIRPYGNHTGNSAPSEADN 300
 DB 241 IKPKNNAEFAAYKENYALMMPYKVKIKPTGEGLVMPDSDIRPYGNHTGNSAPSEADN 300
 QY 301 SHEGYGSDAEVROHROGQP 320
 DB 301 SHEGYGSDAEVROHROGQP 320

RESULT 4
 ID AA274926 standard; protein; 320 AA.
 XX AA274926;
 AC
 XX
 DT 12-SEP-2003 (revised)
 XX
 DT 21-MAR-2000 (first entry)
 XX
 DE *Neisseria gonorrhoeae* ORF 406 protein sequence SEQ ID NO:1326.
 XX
 KW *Neisseria meningitidis*; *Neisseria gonorrhoeae*; antigen; vaccine;
 KW antigenic; diagnostic; immunogenic; infection; meningitis; septicemia;
 KW antibacterial; gene therapy.
 XX
 OS *Neisseria gonorrhoeae*.
 XX
 PN WO9957280-A2.
 XX
 PD 11-NOV-1999.
 XX
 PF 30-APR-1999; 99WO-US009346.
 XX
 PR 01-MAY-1998; 98US-0083758P.
 PR 31-JUL-1998; 98US-0094869P.
 PR 02-SEP-1998; 98US-0098994P.

PR 02-SEP-1998; 98US-0099062P.
 PR 09-OCT-1998; 98US-0103749P.
 PR 09-OCT-1998; 98US-0103794P.
 PR 09-OCT-1998; 98US-0103796P.
 PR 25-FEB-1999; 99US-0121528P.
 XX
 PA (CHIR) CHIRON CORP.
 PA (GENO) INST GENOMIC RES.
 XX
 PI Frazer C, Galeotti C, Grandi G, Hickey E, Masignani V, Mora M;
 PI Petersen J, Pizzo M, Rappuoli R, Ratti G, Scalato E, Scarcelll M;
 PI Tetzelin H, Venter JC;
 XX
 DR WPI: 2000-062150/05.
 DR N-PSDB; AA253688.
 XX
 PT Novel *Neisseria* polypeptides predicted to be useful antigens for
 PT vaccines and diagnostics.
 XX
 PS Claim 2; Page 728; 1453pp; English.
 XX
 CC AA253015 to AA254536, AA254577 to AA254615, and AA274253 to AA275941
 CC represent novel *Neisseria meningitidis* and *N. gonorrhoeae* polynucleotides
 CC and polypeptides. AA254537 to AA254576 and AA254616 to AA254617 represent
 CC PCR primers used in the exemplification of the present invention. The
 CC polypeptides, the polynucleotides, antibodies and compositions of the
 CC invention can be used as vaccines, as diagnostic reagents, and as
 CC immunogenic compositions. The polypeptides can be used in the manufacture
 CC of medicaments for treating or preventing infection due to *Neisseria*
 CC bacteria (e.g. meningitis and septicemia), to detect the presence of
 CC *Neisseria* bacteria, or to raise antibodies. They may also be used to
 CC screen for agonists or antagonists, which may themselves have use as
 CC antibacterial agents. The polynucleotides of the invention may also be
 CC used in gene therapy protocols. (Updated on 12-SEP-2003 to standardise OS
 CC field)

XX Sequence 320 AA;
 SQ

Query Match 99.8%; Score 1641; DB 3; Length 320;
 Best Local Similarity 99.7%; Pred. No. 2.8e-151;
 Matches 319; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRARLLIPILPSVFLISACGTLTGIPSHGGKRRFAVEQELVAASRAAOKMDLQALHGR 60
 DB 1 MRARLLIPILPSVFLISACGTLTGIPSHGGKRRFAVEQELVAASRAAOKMDLQALHGR 60
 QY 61 KVALYIATMGDQSGSLTGRYSIDALIRGEYINSPAVRTDVTYPRYETTAETTSGLTG 120
 DB 61 KVALYIATMGDQSGSLTGRYSIDALIRGEYINSPAVRTDVTYPRYETTAETTSGLTG 120
 QY 121 LTTSLSTINAPALSTGDSGSRSLGNTGMDYNNETLTNPRDTAFSLHVQTVF 180
 DB 121 LTTSLSTINAPALSTGDSGSRSLGNTGMDYNNETLTNPRDTAFSLHVQTVF 180
 QY 181 FLRGIDVVS PANADTVFINIDVFGTIRNRTEMLYNAETLKAQTKLEFPAVDRTNKKLL 240
 DB 181 FLRGIDVVS PANADTVFINIDVFGTIRNRTEMLYNAETLKAQTKLEFPAVDRTNKKLL 240
 QY 241 IKPKNNAEFAAYKENYALMMPYKVKIKPTGEGLVMPDSDIRPYGNHTGNSAPSEADN 300
 DB 241 IKPKNNAEFAAYKENYALMMPYKVKIKPTGEGLVMPDSDIRPYGNHTGNSAPSEADN 300
 QY 301 SHEGYGSDAEVROHROGQP 320
 DB 301 SHEGYGSDAEVROHROGQP 320

RESULT 5
 ID AAB25657 standard; protein; 320 AA.
 XX AAB25657;
 AC
 XX

DT 12-SEP-2003 (revised)
DT 04-DEC-2000 (first entry)
XX
DE N. gonorrhoeae amino acid sequence g406.pep SEQ ID NO:1037.
XX
KW Neisseria meningitidis; Neisseria gonorrhoeae; genome; immunogenic;
KW antigen; vaccine; diagnosis; infection; antibacterial; identification;
XX Meningococcus B; MenB.
XX
OS Neisseria gonorrhoeae.
XX
EN WO200022430-A2.
XX
PD 20-APR-2000.
XX
PF 08-OCT-1999; 99WO-US023573.
XX
PR 09-OCT-1998; 98US-0103794P.
XX 30-APR-1999; 99US-0132068P.
XX
PA (CHIR) CHIRON CORP.
XX
PI Frazer CM, Hickey E, Peterson J, Tettein H, Venter JC;
PI Maignani V, Galeotti C, Mora M, Ratti G, Scarselli M, Scarlato V;
PI Rappuoli R, Pizza M;
XX
DR WPI; 2000-318079/27.
DR N-PSDB; AAA81297.
XX
XX Isolated nucleotide sequences of Neisseria meningitidis which can be used
PT in the diagnosis and treatment of N. meningitidis infection and other
PT Neisserial infections, for example, N.gonorrhoea.
XX
PS Claim 14; Page 108; 1760pp; English.
XX
XX The present invention describes methods of obtaining immunogenic proteins
CC from Neisseria genomic sequences. AAA81453 to AAA82414 represent
CC specifically claimed Neisseria meningitidis genomic DNA sequences;
CC AAA81260 to AAA81303 and AAB25620 to AAB25663 represent Neisseria DNA
CC sequences and their corresponding proteins; AAA81254 to AAA81259 and
CC AAA81304 to AAA81321 represent PCR primers used in the isolation of
CC Neisseria meningitidis DNA sequences; and AAA81322 to AAA81452 represent
CC Neisseria meningitidis MemB polynucleotide ORF sequences, which are all
CC used in the exemplification of the present invention. The nucleic acid
CC sequences, protein sequences, and antibodies against them, can be used in
CC the manufacture of a composition. The composition can be used as a
CC medicament (or in the manufacture of a medicament) for treating,
CC preventing or diagnosing infection due to Neisserial bacteria. For
CC example, some of the identified proteins could be components of vaccines
CC against Meningococcus B; against all serotypes; and/or against all
CC pathogenic Neisseriae. Identification of sequences from the bacterium
CC will also facilitate production of biological probes, particularly
CC organism-specific probes. Attempts to make efficacious Meningococcus B
CC vaccines have failed mainly due to antigen tolerance. Multivalent
CC vaccines have also been tried but none have successfully overcome
CC antigenic variability. The provision of further, complete sequences may
CC provide an opportunity to identify secreted or surface exposed proteins
CC that may be presumed targets for the immune system and which are not
CC antigenically variable or at least more conserved than other more
CC variable regions. (Updated on 12-SEP-2003 to standardise OS field)
XX
SQ Sequence 320 AA;
Query Match 99.8%; Score 1641; DB 3; Length 320;
Best Local Similarity 99.7%; Pred. No.2.8e-151; Indels 0; Gaps 0;
Matches 319; Conservative 1; Mismatches 0;
QY 1 MRARLLIPILFVSFLLSAGTLTGIPSHGGKRFPAVEOELVAASRAAVKMDIQLHGR 60
DB 1 MRARLLIPILFVSFLLSAGTLTGIPSHGGKRFPAVEOELVAASRAAVKMDIQLHGR 60
QY 61 KVALYIATMGDQSGSLTGRYSIDALIRGEYINSPAVRTDYTPRYETTAETTSGLITG 120
|||||

DB 61 KVALYIATMGDQSGSLTGRYSIDALIRGEYINSPAVRTDYTPRYETTAETTSGLITG 120
QY 121 LTTSLSTLNAPALSRSTQSDGSSRSLSGLNIGMGWDYRNELTTNPPDTAFSLHVOYVF 180
DB 121 LTTSLSTLNAPALSRSTQSDGSSRSLSGLNIGMGWDYRNELTTNPPDTAFSLHVOYVF 180
QY 181 FLRGIDVSPANADTDVFINIDVFGTIRNRTENHLNVAETLKQTKLEYFVADRTNKKL 240
DB 181 FLRGIDVSPANADTDVFINIDVFGTIRNRTENHLNVAETLKQTKLEYFVADRTNKKL 240
QY 241 IKPRTNAFEAAVKENYVLMMGPRYKSKIGKPTBGLMWFSDIRPYGNHTGNSAPVEADN 300
DB 241 IKPRTNAFEAAVKENYVLMMGPRYKSKIGKPTBGLMWFSDIQPYGNHTGNSAPVEADN 300
QY 301 SHEGYSDEAVRQHRQGP 320
DB 301 SHEGYSDEAVRQHRQGP 320
RESULT 6
ID AAB58587 standard; protein; 320 AA.
XX
AC AAB58587;
XX
DT 12-SEP-2003 (revised)
DT 13-MAR-2001 (first entry)
XX
DE N. gonorrhoeae amino acid sequence g406.pep SEQ ID NO:77.
XX
XX Neisseria meningitidis; Neisseria gonorrhoeae; immunogenic; vaccine;
KW diagnosis; antigen; detection; infection; gene therapy; antibacterial.
XX
OS Neisseria gonorrhoeae.
XX
EN WO200006791-A1.
XX
PD 09-NOV-2000.
XX
PF 08-MAR-2000; 2000WO-US005928.
XX
PR 30-APR-1999; 99US-0132068P.
PR 08-OCT-1999; 99WO-US023573.
PR 28-FEB-2000; 2000GB-00004695.
XX
PA (CHIR) CHIRON CORP.
PA (GENO-) INST GENOMIC RES.
XX
XX Pizza M, Hickey E, Peterson J, Tettein H, Venter JC;
PI Maignani V, Galeotti C, Mora M, Ratti G, Scarselli M, Scarlato V;
PI Rappuoli R, Frazer CM, Grandi G;
XX
DR WPI; 2000-647603/62.
DR N-PSDB; AAF21582.
XX
PT Neisseria meningitidis B full length genome sequence and open reading
PT frames are used to detect, treat and prevent Neisserial infections.
XX
PS Example 1; Page 109; 692pp; English.
XX
XX The present invention describes the full length genome of Neisseria
CC meningitidis B (NMB). The sequences in AAF21544 and AAF21607 to AAF21613
CC represent fragments of the NMB genomic sequence, as the sequence was too
CC long to go in a record on its own it was split into 8 sequences which
CC overlap each other at the beginning and end of each sequence by 49980 bp
CC (i.e. the last 49980 bp of AAF21544 is repeated at the beginning of
CC AAF21607, the last 49980 bp of AAF21607 are repeated at the beginning of
CC AAF21608, and so on). AAF21545 to AAF21588 encode the Neisseria proteins
CC given in AAB58550 to AAB58593, and AAF21589 to AAF21606 represent PCR
CC primers which are used in the exemplification of the present invention.
CC The NMB genome and fragments from it have antibacterial activity, and can
CC be used in vaccines and gene therapy. Neisseria nucleic acids, proteins
CC and/or antibodies which binds to the proteins can be used in compositions

CC for treating or preventing infection due to *Neisseria* bacteria or as a
CC diagnostic reagent for detecting the presence of *Neisseria* bacteria or
CC of antibodies raised to *Neisseria* bacteria. Computers, computer memory,
CC computer storage medium or computer databases can be used in a search to
CC identify open reading frames (ORFs) or coding sequences within the NMB
CC genome. The DNA sequences provide further opportunities to find antigenic
CC or immunogenic proteins which are more effective in vaccines (Updated on
CC 12-SEP-2003 to standardise OS field)

XX
SQ Sequence 320 AA;

Query Match 99.8%; Score 1641; DB 3; Length 320;
Best Local Similarity 99.7%; Pred. No. 2.8e-151;
Matches 319; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRARLLIPILFSVFLISACGTLTGIPSHGGGRFAVEDELVAASARAANKMDLQALHGR 60
DB 1 MRARLLIPILFSVFLISACGTLTGIPSHGGGRFAVEDELVAASARAANKMDLQALHGR 60
QY 61 KVALYIATMGDQSGSLTGGGRYSIDALLRGEYINSPAVRTDYYPRYETTAETTSGLTG 120
DB 61 KVALYIATMGDQSGSLTGGGRYSIDALLRGEYINSPAVRTDYYPRYETTAETTSGLTG 120
QY 121 LTTSLSTLNAPALSRSTQSDGSSRSGLNIGMGDYRNETLTTNPRDTAFSLHVQTVF 180
DB 121 LTTSLSTLNAPALSRSTQSDGSSRSGLNIGMGDYRNETLTTNPRDTAFSLHVQTVF 180
QY 181 FLRGIDVVS PANADTDVFINIDVFETIRNRTEMHLYNAETLKAQTKLEFAVDRTNKLL 240
DB 181 FLRGIDVVS PANADTDVFINIDVFETIRNRTEMHLYNAETLKAQTKLEFAVDRTNKLL 240
QY 241 IKPKTNAFEAAYKENYALMGPYKYSKGIKPTGELMVFSDIQPYGNHTGNSAPSEADN 300
DB 241 IKPKTNAFEAAYKENYALMGPYKYSKGIKPTGELMVFSDIQPYGNHTGNSAPSEADN 300
QY 301 SHEGYGSDAVALROHROGQP 320
DB 301 SHEGYGSDAVALROHROGQP 320

RESULT 7
ABP76947
ID ABP76947 standard; protein; 320 AA.
XX
AC ABP76947;
XX
DT 07-MAR-2003 (first entry)
XX
DE N. gonorrhoeae amino acid sequence SEQ ID 424.
XX
KW Antibacterial; infection; vaccine; gene therapy.
XX
OS *Neisseria gonorrhoeae*.
XX
PN WO200279243-A2.
XX
PD 10-OCT-2002.
XX
PF 12-FEB-2002; 2002WO-IB002069.
XX
PR 12-FEB-2001; 2001GB-00003424.
XX
PA (CHIR-) CHIRON SPA.
XX
PI Fontana M, Pizze M, Masiagnani V, Monaci E;
XX
DR MPI: 2003-058415/05.
XX
DR N-PSDB; AB237917.
XX
PT New protein from *Neisseria gonorrhoeae*, useful for the manufacture of a
XX
PS medicament for treating or preventing N. gonorrhoeae infection.
XX
PS Disclosure; Page 220; 815pp; English.

XX The present invention relates to proteins from *Neisseria gonorrhoeae*.
CC Also disclosed are the nucleic acid molecules encoding the proteins and
CC antibodies that specifically bind to the proteins. The composition
CC comprising the protein, nucleic acid or antibody is useful for the
CC manufacture of a medicament for treating or preventing N. gonorrhoeae
CC infection, this may be in the form of a vaccine or gene therapy.
CC Sequences given in records ABP76736-ABP81046 represent nucleic acid
CC molecules of the invention

XX
SQ Sequence 320 AA;

Query Match 99.8%; Score 1641; DB 6; Length 320;
Best Local Similarity 99.7%; Pred. No. 2.8e-151;
Matches 319; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRARLLIPILFSVFLISACGTLTGIPSHGGGRFAVEDELVAASARAANKMDLQALHGR 60
DB 1 MRARLLIPILFSVFLISACGTLTGIPSHGGGRFAVEDELVAASARAANKMDLQALHGR 60
QY 61 KVALYIATMGDQSGSLTGGGRYSIDALLRGEYINSPAVRTDYYPRYETTAETTSGLTG 120
DB 61 KVALYIATMGDQSGSLTGGGRYSIDALLRGEYINSPAVRTDYYPRYETTAETTSGLTG 120
QY 121 LTTSLSTLNAPALSRSTQSDGSSRSGLNIGMGDYRNETLTTNPRDTAFSLHVQTVF 180
DB 121 LTTSLSTLNAPALSRSTQSDGSSRSGLNIGMGDYRNETLTTNPRDTAFSLHVQTVF 180
QY 181 FLRGIDVVS PANADTDVFINIDVFETIRNRTEMHLYNAETLKAQTKLEFAVDRTNKLL 240
DB 181 FLRGIDVVS PANADTDVFINIDVFETIRNRTEMHLYNAETLKAQTKLEFAVDRTNKLL 240
QY 241 IKPKTNAFEAAYKENYALMGPYKYSKGIKPTGELMVFSDIQPYGNHTGNSAPSEADN 300
DB 241 IKPKTNAFEAAYKENYALMGPYKYSKGIKPTGELMVFSDIQPYGNHTGNSAPSEADN 300
QY 301 SHEGYGSDAVALROHROGQP 320
DB 301 SHEGYGSDAVALROHROGQP 320

RESULT 8
AAV38538
ID AAV38538 standard; protein; 320 AA.
XX
AC AAV38538;
XX
DT 08-OCT-1999 (first entry)
XX
DE *Neisseria meningitidis* strain B antigen encoded by ORF15.
XX
KW *Neisseria meningitidis*; *Neisseria gonorrhoeae*; antigen; vaccine;
XX
OS *Neisseria meningitidis*; *Neisseria* infection; meningitis; septicemia; gonorrhea.
XX
PN WO9924578-A2.
XX
PD 20-MAY-1999.
XX
PF 09-OCT-1998; 98WO-IB001665.
XX
PR 06-NOV-1997; 97GB-00023516.
XX
PR 14-NOV-1997; 97GB-00024190.
XX
PR 18-NOV-1997; 97GB-00024386.
XX
PR 27-NOV-1997; 97GB-00025158.
XX
PR 10-DEC-1997; 97GB-00026147.
XX
PR 14-JAN-1998; 98GB-00000759.
XX
PR 01-SEP-1998; 98GB-00019016.
XX
PA (CHIR-) CHIRON SPA.
XX
PI Masiagnani V, Rappuoli R, Pizze M, Scarlato V, Grandi G;
XX

XX WPI, 1999-327407/27.
 DR N-PSDB; AAZ12006.
 XX
 PT Proteins from *Neisseria meningitidis* and *N. gonorrhoeae* useful for
 diagnosis, treatment and prevention of infection.
 XX
 PS Claim 4; Page 98; 524pp; English.
 XX
 CC Amino acid sequences AAY38499-43894 represent *Neisseria meningitidis* and
 CC *N. gonorrhoeae* antigenic proteins. They are encoded by open reading
 CC frames (ORFs) AAZ1972-212358. The antigenic proteins, their fragments,
 CC their nucleic acids and antibodies are used for diagnosis, prevention (as
 CC vaccines) or treatment of *Neisseria* infections, such as meningitis,
 CC septicemia and gonorrhea. Both organisms are closely related. Fragments
 CC of the nucleic acids are useful as hybridisation probes and antisense
 CC reagents
 XX
 SQ Sequence 320 AA;
 Query Match 99.3%; Score 1634; DB 2; Length 320;
 Best Local Similarity 99.1%; Pred. No. 1.4e-150;
 Matches 317; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MRARLLIPILFSVFILSACGLTGTGIPSHGGKRFVBOELVAASARAAYKMDLQALHGR 60
 DB 1 MQARLLIPILFSVFILSACGLTGTGIPSHGGKRFVBOELVAASARAAYKMDLQALHGR 60
 QY 61 KVALYIATMGDQSGSLTGRYSIDALIRGEYINSPAVRTDYTPRYETTAETTSGLTG 120
 DB 61 KVALYIATMGDQSGSLTGRYSIDALIRGEYINSPAVRTDYTPRYETTAETTSGLTG 120
 QY 121 LTTSLSTLNAPALSRTOSSDGSRSLSGLNIGMGDYRNETHLTNPRDTAFSLHVOTVF 180
 DB 121 LTTSLSTLNAPALSRTOSSDGSRSLSGLNIGMGDYRNETHLTNPRDTAFSLHVOTVF 180
 QY 181 FLRGIDVSPANADTVFINIDVFGTIRNRTMHLVNAETLKAQTKLEYFAVDRTNKKL 240
 DB 181 FLRGIDVSPANADTVFINIDVFGTIRNRTMHLVNAETLKAQTKLEYFAVDRTNKKL 240
 QY 241 IKPRTNAFEAAYKENYALMMPYKVSIGIKPTGELMVDPSDIRPYGHTGNSAPSEADN 300
 DB 241 IKPRTNAFEAAYKENYALMMPYKVSIGIKPTGELMVDPSDIRPYGHTGNSAPSEADN 300
 QY 301 SHEGYGSDAIVROHROGQP 320
 DB 301 SHEGYGSDAIVROHROGQP 320
 RESULT 9
 AAY74927
 ID AAY74927 standard; protein; 320 AA.
 AC AAY74927;
 XX
 DT 21-MAR-2000 (first entry)
 XX
 DE *Neisseria meningitidis* ORF 406 protein sequence SEQ ID NO:1328.
 XX
 KW *Neisseria meningitidis*; *Neisseria gonorrhoeae*; antigen; vaccine;
 KW antigenic; diagnosis; immunogenic; infection; meningitis; septicemia;
 KW antibacterial; gene therapy.
 XX
 OS *Neisseria meningitidis*.
 XX
 PN WO9957280-A2.
 PD 11-NOV-1999.
 PF 30-APR-1999; 99WO-US009346.
 PR 01-MAY-1998; 98US-0083758P.
 PR 31-JUL-1998; 98US-0094869P.

PR 02-SEP-1998; 98US-0098994P.
 PR 02-SEP-1998; 98US-0099062P.
 PR 09-OCT-1998; 98US-0103749P.
 PR 09-OCT-1998; 98US-0103794P.
 PR 09-OCT-1998; 98US-0103796P.
 PR 25-FEB-1999; 99US-0121528P.
 XX
 PA (CHIR) CHIRON CORP.
 PA (GENO-) INST GENOMIC RES.
 XX
 PI Fraser C, Galeotti C, Grandi G, Hickey E, Maignani V, Mora M,
 PI Petersen J, Pizzar M, Rappuoli R, Ratti G, Scalato E, Scarselli M,
 PI Tettei H, Venter JC;
 XX
 DR WPI; 2000-062150/05.
 DR N-PSDB; AAZ53689.
 XX
 PT Novel *Neisseria* polypeptides predicted to be useful antigens for
 PT vaccines and diagnostics.
 XX
 PS Claim 2; Page 728-729; 1453pp; English.
 XX
 CC AA253015 to AA254536, AA254577 to AA254615, and AAY74253 to AAY75941
 CC represent novel *Neisseria meningitidis* and *N. gonorrhoeae* polynucleotides
 CC and polypeptides. AA254537 to AA254576 and AA254616 to AA25473 represent
 CC PCR primers used in the exemplification of the present invention. The
 CC polypeptides, the polynucleotides, antibodies and compositions of the
 CC invention can be used as vaccines, as diagnostic reagents, and as
 CC immunogenic compositions. The polypeptides can be used in the manufacture
 CC of medicaments for treating or preventing infection due to *Neisseria*
 CC bacteria (e.g. meningitis and septicemia), to detect the presence of
 CC *Neisseria* bacteria, or to raise antibodies. They may also be used to
 CC screen for agonists or antagonists, which may themselves have use as
 CC antibacterial agents. The polynucleotides of the invention may also be
 CC used in gene therapy protocols
 XX
 SQ Sequence 320 AA;
 Query Match 99.3%; Score 1634; DB 3; Length 320;
 Best Local Similarity 99.1%; Pred. No. 1.4e-150;
 Matches 317; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MRARLLIPILFSVFILSACGLTGTGIPSHGGKRFVBOELVAASARAAYKMDLQALHGR 60
 DB 1 MQARLLIPILFSVFILSACGLTGTGIPSHGGKRFVBOELVAASARAAYKMDLQALHGR 60
 QY 61 KVALYIATMGDQSGSLTGRYSIDALIRGEYINSPAVRTDYTPRYETTAETTSGLTG 120
 DB 61 KVALYIATMGDQSGSLTGRYSIDALIRGEYINSPAVRTDYTPRYETTAETTSGLTG 120
 QY 121 LTTSLSTLNAPALSRTOSSDGSRSLSGLNIGMGDYRNETHLTNPRDTAFSLHVOTVF 180
 DB 121 LTTSLSTLNAPALSRTOSSDGSRSLSGLNIGMGDYRNETHLTNPRDTAFSLHVOTVF 180
 QY 181 FLRGIDVSPANADTVFINIDVFGTIRNRTMHLVNAETLKAQTKLEYFAVDRTNKKL 240
 DB 181 FLRGIDVSPANADTVFINIDVFGTIRNRTMHLVNAETLKAQTKLEYFAVDRTNKKL 240
 QY 241 IKPRTNAFEAAYKENYALMMPYKVSIGIKPTGELMVDPSDIRPYGHTGNSAPSEADN 300
 DB 241 IKPRTNAFEAAYKENYALMMPYKVSIGIKPTGELMVDPSDIRPYGHTGNSAPSEADN 300
 QY 301 SHEGYGSDAIVROHROGQP 320
 DB 301 SHEGYGSDAIVROHROGQP 320
 RESULT 10
 AAY75811
 ID AAY75811 standard; protein; 320 AA.
 AC AAY75811;
 XX

CC provide an opportunity to identify secreted or surface exposed proteins
 CC that may be presumed targets for the immune system and which are not
 CC antigenically variable or at least more conserved than other more
 CC variable regions

XX Sequence 320 AA;

Query Match 99.3%; Score 1634; DB 3; Length 320;
 Best Local Similarity 99.1%; Pred. No. 1,4e-150;
 Matches 317; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MRARLLIPILFSVFLSACGTLTGIPSHGGGKRRFAVEQELVAASARAAYKMDLQALHGR 60
 DB 1 MQARLLIPILFSVFLSACGTLTGIPSHGGGKRRFAVEQELVAASARAAYKMDLQALHGR 60
 QY 61 KVALYIATMGDQSGSLTGRYSIDALIRGEYINSFARTDYTPRYETTAETTSGLTG 120
 DB 61 KVALYIATMGDQSGSLTGRYSIDALIRGEYINSFARTDYTPRYETTAETTSGLTG 120
 QY 121 LTTSLSTLNAPALSRTOGSGSRSLGLNIGMGDYNNETLTPRDTAFLSHLVOTVF 180
 DB 121 LTTSLSTLNAPALSRTOGSGSRSLGLNIGMGDYNNETLTPRDTAFLSHLVOTVF 180
 QY 181 FLRGIDVVS PANADTVFINIDVFGTIRNRTTEMLYNAETLKAQTKLEYFAVDRTNKKL 240
 DB 181 FLRGIDVVS PANADTVFINIDVFGTIRNRTTEMLYNAETLKAQTKLEYFAVDRTNKKL 240
 QY 241 IKPKPTNAFEAAYKENYALMMGPYKSKIGKPTGELMVDPSDIRPGNHTGNSAPVEADN 300
 DB 241 IKPKPTNAFEAAYKENYALMMGPYKSKIGKPTGELMVDPSDIRPGNHTGNSAPVEADN 300
 QY 301 SHEGYGSDAVROHROGQP 320
 DB 301 SHEGYGSDAVROHROGQP 320

RESULT 12

AAB58586 ID AAB58586 standard; protein; 320 AA.

XX AAB58586;

DT 13-MAR-2001 (first entry)

XX N. meningitidis amino acid sequence m406.pap SEQ ID NO:75.

KW Neisseria meningitidis; Neisseria gonorrhoeae; immunogenic; vaccine;
 KW diagnosis; antigen; detection; infection; gene therapy; antibacterial.

XX Neisseria meningitidis.

OS WO200066791-A1.

PD 09-NOV-2000.

PP 08-MAR-2000; 2000WO-US005928.

XX 30-APR-1999; 99US-0132068P.

PR 08-OCT-1999; 99WO-US023573.

PR 28-FEB-2000; 2000GB-00004655.

XX (CHIR) CHIRON CORP.

PA (GENO-) INST GENOMIC RES.

PI Pizsa M, Hickey E, Peterson J, Tettelin H, Venter JC,
 PI Maignani V, Galeotti C, Mora M, Ratti G, Scariselli M, Scarlato V,
 PI Rappelli R, Frazer CM, Grandi G;

XX WPI; 2000-647603/62.

DR N-PSDB; AAF21581.

XX Neisseria meningitidis B full length genome sequence and open reading
 PT frames are used to detect, treat and prevent Neisseria infections.

XX Example 1; Page 108; 692pp; English.

CC The present invention describes the full length genome of Neisseria
 CC meningitidis B (NMB). The sequences in AAF21544 and AAF21607 to AAF21613
 CC represent fragments of the NMB genomic sequence, as the sequence was too
 CC long to go in a record on its own it was split into 8 sequences which
 CC overlap each other at the beginning and end of each sequence by 49980 bp
 CC (i.e. the last 49980 bp of AAF21544 is repeated at the beginning of
 CC AAF21607, the last 49980 bp of AAF21607 are repeated at the beginning of
 CC AAF21608, and so on). AAF21545 to AAF21588 encode the Neisseria proteins
 CC given in AAB58550 to AAB58593, and AAF21589 to AAF21606 represent PCR
 CC primers which are used in the exemplification of the present invention.
 CC The NMB genome and fragments from it have antibacterial activity, and can
 CC be used in vaccines and gene therapy. Neisseria nucleic acids, proteins
 CC and/or antibodies which binds to the proteins can be used in compositions
 CC for treating or preventing infection due to Neisseria bacteria or as a
 CC diagnostic reagent for detecting the presence of Neisseria bacteria or
 CC of antibodies raised to Neisseria bacteria. Computers, computer memory,
 CC computer storage medium or computer databases can be used in a search to
 CC identify open reading frames (ORFs) or coding sequences within the NMB
 CC genome. The DNA sequences provide further opportunities to find antigenic
 CC or immunogenic proteins which are more effective in vaccines

XX Sequence 320 AA;

Query Match 99.3%; Score 1634; DB 3; Length 320;
 Best Local Similarity 99.1%; Pred. No. 1,4e-150;
 Matches 317; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MRARLLIPILFSVFLSACGTLTGIPSHGGGKRRFAVEQELVAASARAAYKMDLQALHGR 60
 DB 1 MQARLLIPILFSVFLSACGTLTGIPSHGGGKRRFAVEQELVAASARAAYKMDLQALHGR 60
 QY 61 KVALYIATMGDQSGSLTGRYSIDALIRGEYINSFARTDYTPRYETTAETTSGLTG 120
 DB 61 KVALYIATMGDQSGSLTGRYSIDALIRGEYINSFARTDYTPRYETTAETTSGLTG 120
 QY 121 LTTSLSTLNAPALSRTOGSGSRSLGLNIGMGDYNNETLTPRDTAFLSHLVOTVF 180
 DB 121 LTTSLSTLNAPALSRTOGSGSRSLGLNIGMGDYNNETLTPRDTAFLSHLVOTVF 180
 QY 181 FLRGIDVVS PANADTVFINIDVFGTIRNRTTEMLYNAETLKAQTKLEYFAVDRTNKKL 240
 DB 181 FLRGIDVVS PANADTVFINIDVFGTIRNRTTEMLYNAETLKAQTKLEYFAVDRTNKKL 240
 QY 241 IKPKPTNAFEAAYKENYALMMGPYKSKIGKPTGELMVDPSDIRPGNHTGNSAPVEADN 300
 DB 241 IKPKPTNAFEAAYKENYALMMGPYKSKIGKPTGELMVDPSDIRPGNHTGNSAPVEADN 300
 QY 301 SHEGYGSDAVROHROGQP 320
 DB 301 SHEGYGSDAVROHROGQP 320

RESULT 13

AAY38539 ID AAY38539 standard; protein; 320 AA.

XX AAY38539;

DT 08-OCT-1999 (first entry)

XX Neisseria meningitidis strain A antigen encoded by ORF15.

KW Neisseria meningitidis; Neisseria gonorrhoeae; antigen; vaccine;
 KW treatment; Neisseria infection; meningitis; septicemia; gonorrhea.

XX Neisseria meningitidis.

OS WO9924578-A2.

XX 20-MAY-1999.

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XX 09-OCT-1998; 98WO-1B001665.
PR 06-NOV-1997; 97GB-00023516.
XX 14-NOV-1997; 97GB-00024190.
PR 18-NOV-1997; 97GB-00024386.
XX 27-NOV-1997; 97GB-00025158.
PR 10-DEC-1997; 97GB-00026147.
XX 14-JAN-1998; 98GB-00000759.
PR 01-SEP-1998; 98GB-00019016.
XX (CHIR-) CHIRON SPA.
XX Masignani V, Rappuoli R, Pizza M, Scarlato V, Grandi G;
PI WPI; 1999-327407/27.
XX N-PSDB; AA212007.
XX Proteins from Neisseria meningitidis and N. gonorrhoeae useful for
PT diagnosis, treatment and prevention of infection.
XX Claim 4; Page 98-99; 524pp; English.
XX Amino acid sequences AAY38499-Y38944 represent Neisseria meningitidis and
CC N. gonorrhoeae antigenic proteins. They are encoded by open reading
CC frames (ORFs) AA211972-212358. The antigenic proteins, their fragments,
CC their nucleic acids and antibodies are used for diagnosis, prevention (as
CC vaccines) or treatment of Neisseria infections, such as meningitis,
CC septicemia and gonorrhea. Both organisms are closely related. Fragments
CC of the nucleic acids are useful as hybridisation probes and antisense
CC reagents
XX SQ
XX Sequence 320 AA;
XX Query Match 98.7%; Score 1624; DB 2; Length 320;
XX Best Local Similarity 98.4%; Pred. No. 1.3e-149;
XX Matches 315; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
QY 1 MRARLLIPILFSVFLSACGTLTGIPSHGGGRRFAVEDELVAASARAAYKMDLQALHGR 60
DB 1 MOARLLIPILFSVFLSACGTLTGIPSHGGGRRFAVEDELVAASARAAYKMDLQALHGR 60
QY 61 KVALYIATMGDGGSLTGGRRYSIDALIRGEYINSPAVRTDYYTPRYETTAETTSGLTGG 120
DB 61 KVALYIATMGDGGSLTGGRRYSIDALIRGEYINSPAVRTDYYTPRYETTAETTSGLTGG 120
QY 121 LTTSLSTLNAPALSRTOSSDGSRRSLGINTGMDYRNELTTNPRDTAFSLHVOYVF 180
DB 121 LTTSLSTLNAPALSRTOSSDGSRRSLGINTGMDYRNELTTNPRDTAFSLHVOYVF 180
QY 121 LTTSLSTLNAPALSRTOSSDGSRRSLGINTGMDYRNELTTNPRDTAFSLHVOYVF 180
DB 121 LTTSLSTLNAPALSRTOSSDGSRRSLGINTGMDYRNELTTNPRDTAFSLHVOYVF 180
QY 181 FLRGIDVVSANADTDVFINIDVFGTIRNRTEMHLYNAETLKAOQKLEYFAVDRTNKKLL 240
DB 181 FLRGIDVVSANADTDVFINIDVFGTIRNRTEMHLYNAETLKAOQKLEYFAVDRTNKKLL 240
QY 241 IKPKTNAFEAAYKENVALMGMGPYKSKIKPTEGLMVDPSDIQPYGNHNGNSAPSV EADN 300
DB 241 IKPKTNAFEAAYKENVALMGMGPYKSKIKPTEGLMVDPSDIQPYGNHNGNSAPSV EADN 300
QY 301 SHEGYGSDAEVQRHRCQP 320
DB 301 SHEGYGSDAEVQRHRCQP 320
XX RESULT 14
XX AAY74928
XX ID AAY74928 standard; protein; 320 AA.
XX AC AAY74928;
XX 21-MAR-2000 (first entry)
XX DT
XX DE Neisseria meningitidis ORF 406 protein sequence SEQ ID NO:1330.
XX

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KW Neisseria meningitidis; Neisseria gonorrhoeae; antigen; vaccine;
KM antigenic; diagnosis; immunogenic; infection; meningitis; septicemia;
KW antibacterial; gene therapy.
XX Neisseria meningitidis.
XX WO957280-A2.
XX 11-NOV-1999.
XX 30-APR-1999; 99WO-US009346.
XX 01-MAY-1998; 98US-0083758P.
PR 31-JUL-1998; 98US-0094869P.
XX 02-SEP-1998; 98US-0096994P.
PR 02-SEP-1998; 98US-0099062P.
XX 09-OCT-1998; 98US-0103749P.
PR 09-OCT-1998; 98US-0103794P.
XX 09-OCT-1998; 98US-0103796P.
PR 25-FEB-1999; 99US-0121528P.
XX (CHIR-) CHIRON CORP.
XX (GENO-) INST GENOMIC RES.
XX Fraser C, Galeotti C, Grandi G, Hickey E, Masignani V, Mora M;
PI Petersen J, Pizza M, Rappuoli R, Ratti G, Scarlato V, Scarselli M;
PI Tettelin H, Venter JC;
XX WPI; 2000-062150/05.
XX N-PSDB; AA253690.
XX Novel Neisseria polypeptides predicted to be useful antigens for
PT vaccines and diagnostics.
XX Claim 2; Page 730; 1453pp; English.
XX AA253015 to AA254536, AA254577 to AA254615, and AAY74253 to AAY75941
XX represent novel Neisseria meningitidis and N. gonorrhoeae polynucleotides
XX and polypeptides; AA254537 to AA254576 and AA254616 to AA254773 represent
XX PCR primers used in the exemplification of the present invention. The
XX CC polypeptides can be used as vaccines, antibodies and compositions of the
XX CC invention can be used as vaccines, as diagnostic reagents, and as
XX CC immunogenic compositions. The polypeptides can be used in the manufacture
XX CC of medicaments for treating or preventing infection due to Neisseria
XX CC bacteria (e.g. meningitis and septicemia), to detect the presence of
XX CC Neisseria bacteria, or to raise antibodies. They may also be used to
XX CC screen for agonists or antagonists, which may themselves have use as
XX CC antibacterial agents. The polynucleotides of the invention may also be
XX CC used in gene therapy protocols
XX SQ
XX Sequence 320 AA;
XX Query Match 98.7%; Score 1624; DB 3; Length 320;
XX Best Local Similarity 98.4%; Pred. No. 1.3e-149;
XX Matches 315; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
QY 1 MRARLLIPILFSVFLSACGTLTGIPSHGGGRRFAVEDELVAASARAAYKMDLQALHGR 60
DB 1 MOARLLIPILFSVFLSACGTLTGIPSHGGGRRFAVEDELVAASARAAYKMDLQALHGR 60
QY 61 KVALYIATMGDGGSLTGGRRYSIDALIRGEYINSPAVRTDYYTPRYETTAETTSGLTGG 120
DB 61 KVALYIATMGDGGSLTGGRRYSIDALIRGEYINSPAVRTDYYTPRYETTAETTSGLTGG 120
QY 121 LTTSLSTLNAPALSRTOSSDGSRRSLGINTGMDYRNELTTNPRDTAFSLHVOYVF 180
DB 121 LTTSLSTLNAPALSRTOSSDGSRRSLGINTGMDYRNELTTNPRDTAFSLHVOYVF 180
QY 121 LTTSLSTLNAPALSRTOSSDGSRRSLGINTGMDYRNELTTNPRDTAFSLHVOYVF 180
DB 121 LTTSLSTLNAPALSRTOSSDGSRRSLGINTGMDYRNELTTNPRDTAFSLHVOYVF 180
QY 181 FLRGIDVVSANADTDVFINIDVFGTIRNRTEMHLYNAETLKAOQKLEYFAVDRTNKKLL 240
DB 181 FLRGIDVVSANADTDVFINIDVFGTIRNRTEMHLYNAETLKAOQKLEYFAVDRTNKKLL 240
QY 181 FLRGIDVVSANADTDVFINIDVFGTIRNRTEMHLYNAETLKAOQKLEYFAVDRTNKKLL 240
DB 181 FLRGIDVVSANADTDVFINIDVFGTIRNRTEMHLYNAETLKAOQKLEYFAVDRTNKKLL 240
QY 241 IKPKTNAFEAAYKENVALMGMGPYKSKIKPTEGLMVDPSDIQPYGNHNGNSAPSV EADN 300

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Db      241  |||
241  IKPTNAFEAAKYKENVALMMGPYKVSKGIKPTBGLMVFSDIQPYGNHMGNSAPSEVADN 300
QY      301  |||
301  SHEGYGYSDEAVRHRROGQP 320
Db      301  |||
301  SHEGYGYSDEAVRHRROGQP 320

RESULT 15
AAV75813
ID  AAV75813 standard; protein; 320 AA.
XX
AC  AAV75813;
XX
DT  21-MAR-2000 (first entry)
XX
DE  Neisseria meningitidis ORF 406 protein sequence SEQ ID NO:3114.
XX
KW  Neisseria meningitidis; Neisseria gonorrhoeae; antigen; vaccine;
KW  antigenic; diagnosis; immunogenic; infection; meningitis; septicemia;
KW  antibacterial; gene therapy.
XX
OS  Neisseria meningitidis.
XX
PN  W09957280-A2.
XX
PD  11-NOV-1999.
XX
PF  30-APR-1999; 99WO-US009346.
XX
PR  01-MAY-1998; 98US-0083758P.
PR  31-JUL-1998; 98US-0094869P.
PR  02-SEP-1998; 98US-0098994P.
PR  02-SEP-1998; 98US-0099062P.
PR  09-OCT-1998; 98US-0103749P.
PR  09-OCT-1998; 98US-0103794P.
PR  09-OCT-1998; 98US-0103796P.
PR  25-FEB-1999; 99US-0121528P.
XX
PA  (CHIR ) CHIRON CORP.
PA  (GENO-) INST GENOMIC RES.
XX
PI  Fraser C, Galeotti C, Grandi G, Hickey E, Masignani V, Mora M;
PI  Petersen J, Pizzo M, Rappuoli R, Ratti G, Scalato E, Scarselli M;
PI  Tettelin H, Venter JC;
XX
DR  WPI; 2000-062150/05.
DR  N-PSDB; AAZ54615.
XX
PT  Novel Neisserial polypeptides predicted to be useful antigens for
PT  vaccines and diagnostics.
XX
PS  Example 1, Page 110-111; 1453pp; English.
XX
CC  AAZ53015 to AAZ54536, AAZ54577 to AAZ54615, and AAV74253 to AAV75941
CC  represent novel Neisseria meningitis and N. gonorrhoeae polynucleotides
CC  and polypeptides. AAZ54537 to AAZ54576 and AAZ54616 to AAZ5473 represent
CC  PCR primers used in the exemplification of the present invention. The
CC  polypeptides, the polynucleotides, antibodies and compositions of the
CC  invention can be used as vaccines, as diagnostic reagents, and as
CC  immunogenic compositions. The polypeptides can be used in the manufacture
CC  of medicaments for treating or preventing infection due to Neisserial
CC  bacteria (e.g. meningitis and septicemia), to detect the presence of
CC  Neisseria bacteria, or to raise antibodies. They may also be used to
CC  screen for agonists or antagonists, which may themselves have use as
CC  antibacterial agents. The polynucleotides of the invention may also be
CC  used in gene therapy protocols
XX
SO  Sequence 320 AA;

```

```

Query Match      98.7%; Score 1624; DB 3; Length 320;
Best Local Similarity 98.4%; Pred. No. 1.3e-149;
Matches 315; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

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QY      1  MRARLLIPILFSVFILSACGLTGI PSHGGKRFPAVEQELVAASARAAXVDMIDLQALHGR 60
1  :|||||
Db      1  MQARLLIPILFSVFILSACGLTGI PSHGGKRFPAVEQELVAASARAAXVDMIDLQALHGR 60
QY      61  KVALYIATMGDQSGSLTGGRYSIDALI RGEYINS PAVRDYTY PRYETTAETTSGLTG 120
61  KVALYIATMGDQSGSLTGGRYSIDALI RGEYINS PAVRDYTY PRYETTAETTSGLTG 120
Db      61  KVALYIATMGDQSGSLTGGRYSIDALI RGEYINS PAVRDYTY PRYETTAETTSGLTG 120
QY      121  LTSTSLTNAPALSRTQSDSGSRSLGLNIGMGDYRNELTTPRDTAFLSHLVOTVF 180
121  LTSTSLTNAPALSRTQSDSGSRSLGLNIGMGDYRNELTTPRDTAFLSHLVOTVF 180
Db      121  LTSTSLTNAPALSRTQSDSGSRSLGLNIGMGDYRNELTTPRDTAFLSHLVOTVF 180
QY      181  FLRGIDVSPAMADTDVFINIDVFGTIRNRTTMLVNAETLKAQTKLEYFAVDRTNKKL 240
181  FLRGIDVSPAMADTDVFINIDVFGTIRNRTTMLVNAETLKAQTKLEYFAVDRTNKKL 240
Db      181  FLRGIDVSPAMADTDVFINIDVFGTIRNRTTMLVNAETLKAQTKLEYFAVDRTNKKL 240
QY      241  IKPTNAFEAAKYKENVALMMGPYKVSKGIKPTBGLMVFSDIRPYGNHTGNSAPSEADN 300
241  IKPTNAFEAAKYKENVALMMGPYKVSKGIKPTBGLMVFSDIRPYGNHTGNSAPSEADN 300
Db      241  IKPTNAFEAAKYKENVALMMGPYKVSKGIKPTBGLMVFSDIQPYGNHMGNSAPSEADN 300
QY      301  SHEGYGYSDEAVRHRROGQP 320
301  SHEGYGYSDEAVRHRROGQP 320
Db      301  SHEGYGYSDEAVRHRROGQP 320
301  SHEGYGYSDEAVRHRROGQP 320

```

Search completed: August 18, 2005, 22:48:18
Job time : 131 secs

A:Adhesin: MafA2_NMA2112 [imported] - Neisseria meningitidis (strain Z2491 serogroup A)
C:Species: Neisseria meningitidis
C>Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 09-Jul-2004
C:Accession: G81782
R:Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel,
J.; Holtzoyd, S.; Jørgensen, R.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream,
Nature 404, 502-506, 2000
A>Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491.
A:Reference number: AB1775; PMID:20222556; PMID:10761919
A:Accession: G81782
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-313 <PAR>
A:Cross-references: UNIPROT:Q9J5W0; GB:A1162758; GB:A1157959; NID:g7380672; PIDD:CAE85322
A:Experimental source: serogroup A, strain Z2491
C:Genetics:
A:Gene: mafA2; NMA2112
A:Superfamily: Neisseria adhesin mafa

QY 74 SGLSTGRYSIDLLI-----RGEX-----INSPAVRIDYTPRXYETAAETSGG 117
|||::|||
Db 232 NGSIITTEKYP-DRLANPVVVKKKGNKKRVSDVDTLNKAACPXSFLIPRIDRLVESTSG- 289

QY 118 LTGLTSLSTLANPALSRTOSDSGSKSLGLNLIGMGDYNRETLTNP-----RDTA 170
|||::|||
Db 290 ----NNALSTRSSPC--RSENDGSVHRRYRGKVFGGGGTNLNVKLNPAAKYRFVRVSGE 343

QY 171 FLSHLVOTVFPLRGIDVSPANADTDVFINIDVFG-----TIIRRTMHLVNAETLK 222
|||::|||
Db 344 FLAGVPVPH----RGIEENPKARN-----SIDNGVTAKORLSTAINRRVVALNRPFPSRS 393

QY 223 AQTLEFYFAVDPRNKULLIKPTNAPAAAYKE 254
:::|||
Db 394 TNKCWAIFYDVLRGNKF--EWTTQGEAEOE 422

RESULT 5
ABI452
chitinase B homolog lin0153 [imported] - *Listeria innocua* (strain Ctip11262)
C/Species: *Listeria innocua*

Qy 255 NYALMGPKYKSGIK 270
| : : : :
Db 2706 NDSLATLDFSLRLKX 2721

RESULT 8

AB1088

chitinase B homolog lmo0105 [imported] - *Listeria monocytogenes* (strain EGD-e)C:Species: *Listeria monocytogenes*

C:Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004

C:Accession: AB1088

R:Glaser, P.; Frangoul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker, J.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurge, O.; Entian, K.D.; Fsihl, H.

D.; Jones, L.M.; Karst, U.

Science 294, 849-852, 2001

A:Authors: Kretz, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maicournam, A.; Ma

ok, C.; Schuener, T.; Simoes, N.; Tietze, A.; Vazquez-Boland, J.A.; Voss, H.; Wehlend, A.

A:Title: Comparative genomics of *Listeria* species.

A:Reference number: AB1077; MUID:21537279; PMID:11679669

A:Accession: AB1088

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-756 <GLA>

A:Cross-references: UNIPROT:Q8VAL3; GB:NC_003210; PIDN:G16409464; GSPDB:

A:Experimental source: strain EGD-e

C:Genetics:

A:Gene: lmo0105

C:Superfamily: chitinase with C-terminal chitin-binding domain

Query Match 6.0%; Score 99.5; DB 2; Length 756;

Best Local Similarity 22.7%; Pred. No. 6.7;

Matches 73; Conservative 37; Mismatches 11; Indels 10; Gaps 16;

Qy 18 ACGLTGTGPGSGKRAVEBELVAASRAVQMDLQALHGRKVALYATMGQSSSL 77
| : : : : :
Db 321 AAGDTALPG-----LFQAELKTNKADGSLTYGANNENPIKT---GGQGR 363
78 TGGY---SIDAL-----IRGEYNSPAVRTDYTPRYETATETSSGLTG 120
364 AGGVWATRSIDALAKKPTLKEYWDDTKAKPYLSKEGEYTT----- 407
Db 121 LTTSLSLTMAPALSRTOSSGSSRSISGLTNGMGDY---ENETLTTPNPDPAFLSHLVQ 177
408 -----DNTSISGYKAYQVKNQNGIMSWQSDKXTTSTKRDE--LTAKIK 452
Qy 178 TVPFLRGIDVSPNADTDVINIDVFTINRRTMHLNNAETLKAQTKLEYFAVDRTNK 237
| : : : : :
Db 453 TGLF--GTSAL-PONAIT--YANLNVAATVPKPSYSENGVYEITITNNEK----ADETNE 502
Qy 238 KLLIKPTNAPFAA-----YKENVALMGPKYKSGIKPTG--LMVDFSDI----- 282
503 --VKSSTELSEHYKLPKFTYFPVAKAGETLTAGDYKA--GYTTSGGNTVVDLASYDAQO 558
Qy 283 ---RPGNHTGSNAPSVEADN 300
559 IPGASVTFRLKSSASSVDVAN 580

RESULT 9

E75278

hypothetical protein - *Deinococcus radiodurans* (strain R1)C:Species: *Deinococcus radiodurans*

C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004

C:Accession: E75278

R:White, O.; Eisten, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;

S.; Shen, M.; Yamachayan, J.J.; Lam, P.; McDonald, L.; Uterback, T.; Zalewski, C.; Ma

Science 286, 1571-1577, 1999

A:Title: Genome sequence of the radioresistant bacterium *Deinococcus radiodurans* R1.

A:Reference number: A75250; MUID:20036896; PMID:10567266

A:Accession: E75278

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-874 <WHI>
A:Cross-references: UNIPROT:Q9RRU3; GB:AE002070; GB:AE000513; NID:G6460209; PIDN:AAF11946
A:Experimental source: strain R1
C:Genetics:
A:Gene: DR2392
A:Map position: 1

Query Match 6.0%; Score 99.5; DB 2; Length 874;

Best Local Similarity 24.3%; Pred. No. 8.2;

Matches 66; Conservative 24; Mismatches 11; Indels 7; Gaps 10;

Qy 30 GGRFAVEQELVAAS-----ARAAVQMDLQALHGRKVALYATMGQSSSLTG 80
| : : : : :
Db 604 GNVAVAYGVELPPTASGAGNARFCATTTLLPLNDRTALTNLGNVLY-----DVGKAPEGA 658
Qy 81 -----RSIDALIRGEYNSPAVRTDYTPRYETATETSSGLTGLTSLTMAPALSR 135
| : : : : :
Db 659 TGADINKTKTRL-----SATVGTDVSYRGDTGFGVVLRGQSVTDELTLNAGGTAE 711
Qy 136 TQSDGSGSRSLG-----LNTGMDYNNETLTTPNPDPAFLSHLVQTVFPFGIDVV 188
Db 712 FQGRREERLELGYAYGRSLSSIGRYVAGSLAGKPE--LSFVSAAVRLP----- 763
Qy 189 SPANADTVFINIDVFTINRRTMHLNNAETLKAQTKLEYFAVDRTN---KKLIK 243
| : : : : :
Db 764 -----NMVVRGVSRTQLDDRDSFTLQGMWLGSSVYLTDLAVGAMARALTPA 812
Qy 244 -KTNAPFAAKENKALMGPKYKSGIKPTG 274
| : : : : :
Db 813 SQTTLF-----GYGVSVPPLPG 831

RESULT 10

S26365

surface-layer protein precursor - *Thermus aquaticus*

N/Alternate names: PilO protein; S-layer protein

C:Species: *Thermus aquaticus*

C:Date: 22-Nov-1993 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004

C:Accession: S26365; A47024; S69792

R:Jasa, I.; de Grado, M.; de Pedro, M.A.; Berenguer, J.

J. Bacteriol. 174, 6424-6431, 1992

A:Title: Development of *Thermus*-*Escherichia* shuttle vectors and their use for expression

A:Reference number: S26365; MUID:93015692; PMID:1400194

A:Accession: S26365

A:Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-917 <LAS>

A:Cross-references: UNIPROT:P35830; EMBL:X57333; NID:G48277; PIDN:CAA40609.1; PID:G48278

A:Experimental source: strain HB8

A>Note: the nucleotide sequence was submitted to the EMBL Data Library, January 1991

R:Parado, M.M.; de Pedro, M.A.; Berenguer, J.

J. Bacteriol. 174, 7458-7462, 1992

A:Title: Sequence of the S-layer gene of *Thermus thermophilus* HB8 and functionality of it

A:Reference number: A47024; MUID:93054364; PMID:1429468

A:Accession: A47024

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-200, 'A', 202-917 <FAR>

A:Experimental source: strain HB8

A>Note: sequence inconsistent with the nucleotide translation

A>Note: sequence extracted from NCBI backbone (NCBI:118097, NCBI:118098)

R:Fernandez-Herrero, L.A.; Badet-Denisot, M.A.; Badet, B.; Berenguer, J.

Mol. Microbiol. 17, 1-12, 1995

A:Title: *gms* of *Thermus thermophilus* HB8: an essential gene for cell-wall synthesis ide

A:Reference number: S69792; MUID:96020657; PMID:7476196

A:Accession: S69792

A:Molecule type: DNA

A:Residues: 1-11 <FER>

A:Cross-references: EMBL:U17352; NID:G1184042; PIDN:AAA86987.1; PID:G1184043

A:Experimental source: strain HB8

A>Note: the source is designated as *Thermus thermophilus*

22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100 101 102 103 104 105 106 107 108 109 110 111 112 113 114 115 116 117 118 119 120 121 122 123 124 125 126 127 128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144 145 146 147 148 149 150 151 152 153 154 155 156 157 158 159 160 161 162 163 164 165 166 167 168 169 170 171 172 173 174 175 176 177 178 179 180 181 182 183 184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200 201 202 203 204 205 206 207 208 209 210 211 212 213 214 215 216 217 218 219 220 221 222 223 224 225 226 227 228 229 230 231 232 233 234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252 253 254 255 256 257 258 259 260 261 262 263 264 265 266 267 268 269 270 271 272 273 274 275 276 277 278 279 280 281 282 283 284 285 286 287 288 289 290 291 292 293 294 295 296 297 298 299 300 301 302 303 304 305 306 307 308 309 310 311 312 313 314 315 316 317 318 319 320 321 322 323 324 325 326 327 328 329 330 331 332 333 334 335 336 337 338 339 340 341 342 343 344 345 346 347 348 349 350 351 352 353 354 355 356 357 358 359 360 361 362 363 364 365 366 367 368 369 370 371 372 373 374 375 376 377 378 379 380 381 382 383 384 385 386 387 388 389 390 391 392 393 394 395 396 397 398 399 400 401 402 403 404 405 406 407 408 409 410 411 412 413 414 415 416 417 418 419 420 421 422 423 424 425 426 427 428 429 430 431 432 433 434 435 436 437 438 439 440 441 442 443 444 445 446 447 448 449 450 451 452 453 454 455 456 457 458 459 460 461 462 463 464 465 466 467 468 469 470 471 472 473 474 475 476 477 478 479 480 481 482 483 484 485 486 487 488 489 490 491 492 493 494 495 496 497 498 499 500 501 502 503 504 505 506 507 508 509 510 511 512 513 514 515 516 517 518 519 520 521 522 523 524 525 526 527 528 529 530 531 532 533 534 535 536 537 538 539 540 541 542 543 544 545 546 547 548 549 550 551 552 553 554 555 556 557 558 559 560 561 562 563 564 565 566 567 568 569 570 571 572 573 574 575 576 577 578 579 580 581 582 583 584 585 586 587 588 589 590 591 592 593 594 595 596 597 598 599 600 601 602 603 604 605 606 607 608 609 610 611 612 613 614 615 616 617 618 619 620 621 622 623 624 625 626 627 628 629 630 631 632 633 634 635 636 637 638 639 640 641 642 643 644 645 646 647 648 649 650 651 652 653 654 655 656 657 658 659 660 661 662 663 664 665 666 667 668 669 670 671 672 673 674 675 676 677 678 679 680 681 682 683 684 685 686 687 688 689 690 691 692 693 694 695 696 697 698 699 700 701 702 703 704 705 706 707 708 709 710 711 712 713 714 715 716 717 718 719 720 721 722 723 724 725 726 727 728 729 730 731 732 733 734 735 736 737 738 739 740 741 742 743 744 745 746 747 748 749 750 751 752 753 754 755 756 757 758 759 760 761 762 763 764 765 766 767 768 769 770 771 772 773 774 775 776 777 778 779 780 781 782 783 784 785 786 787 788 789 790 791 792 793 794 795 796 797 798 799 800 801 802 803 804 805 806 807 808 809 810 811 812 813 814 815 816 817 818 819 820 821 822 823 824 825 826 827 828 829 830 831 832 833 834 835 836 837 838 839 840 841 842 843 844 845 846 847 848 849 850 851 852 853 854 855 856 857 858 859 860 861 862 863 864 865 866 867 868 869 870 871 872 873 874 875 876 877 878 879 880 881 882 883 884 885 886 887 888 889 890 891 892 893 894 895 896 897 898 899 900 901 902 903 904 905 906 907 908 909 910 911 912 913 914 915 916 917 918 919 920 921 922 923 924 925 926 927 928 929 930 931 932 933 934 935 936 937 938 939 940 941 942 943 944 945 946 947 948 949 950 951 952 953 954 955 956 957 958 959 960 961 962 963 964 965 966 967 968 969 970 971 972 973 974 975 976 977 978 979 980 981 982 983 984 985 986 987 988 989 990 991 992 993 994 995 996 997 998 999 1000 1001 1002 1003 1004 1005 1006 1007 1008 1009 1010 1011 1012 1013 1014 1015 1016 1017 1018 1019 1020 1021 1022 1023 1024 1025 1026 1027 1028 1029 1030 1031 1032 1033 1034 1035 1036 1037 1038 1039 1040 1041 1042 1043 1044 1045 1046 1047 1048 1049 1050 1051

Job time : 63 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 18, 2005, 22:29:44 ; Search time 129 Seconds
(without alignments)
1270.274 Million cell updates/sec

Title: US-10-617-835-4

Perfect score: 1645

Sequence: 1 MRARLLIPILFSLVFLSACG.....SHEGYGSDAIVRHRQGP 320

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot 03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1645	100.0	320	2 Q9X6P2	Q9X6P2 neisseria g
2	1624	98.7	320	2 Q9JWK7	Q9JWK7 neisseria m
3	1029	62.6	313	2 Q9J544	Q9J544 neisseria m
4	1026	62.4	313	2 Q9J5W0	Q9J5W0 neisseria m
5	122.5	7.4	511	2 Q8VP63	Q8VP63 mycobacteri
6	117.5	7.1	729	2 Q6NP01	Q6NP01 drosophila
7	117.5	7.1	1250	2 Q02434	Q02434 drosophila
8	117.5	7.1	1250	2 Q9VY88	Q9VY88 drosophila
9	117.5	7.1	1250	2 Q961R2	Q961R2 drosophila
10	114.5	7.0	627	2 Q8KG07	Q8KG07 chlorobium
11	111.5	6.8	3552	2 Q8XSD6	Q8XSD6 raietonia s
12	109	6.6	874	2 Q6G428	Q6G428 bartonella
13	107	6.5	684	2 Q6BCF8	Q6BCF8 lyobacter
14	105.5	6.4	731	2 Q6AVK7	Q6AVK7 oryza sativ
15	104	6.3	863	2 Q9SKF9	Q9SKF9 arabidopsis
16	102.5	6.2	756	2 Q9ZPF3	Q9ZPF3 plasmodium
17	102.5	6.2	1240	2 Q7RS47	Q7RS47 listeria in
18	102.5	6.2	1265	2 Q8EV72	Q8EV72 mycoplasma
19	102	6.2	1004	2 Q54455	Q54455 serratia ma
20	101	6.1	429	2 Q7BRX0	Q7BRX0 anopheles g
21	101	6.1	545	2 Q70LL8	Q70LL8 escherichia
22	101	6.1	1326	2 Q70LB8	Q70LB8 plasmodium
23	101	6.1	3346	2 Q7WN54	Q7WN54 bordetella
24	100.5	6.1	496	2 Q6AN08	Q6AN08 bacteroides
25	100.5	6.1	615	2 Q8J0W6	Q8J0W6 cryptococcu
26	100.5	6.1	1096	2 Q8BKW6	Q8BKW6 mus musculu
27	100	6.1	1035	2 Q33372	Q33372 neisseria g
28	100	6.1	3167	2 Q17464	Q17464 caenorhabdi
29	99.5	6.0	756	2 Q8VAL3	Q8VAL3 listeria mo
30	99.5	6.0	874	2 Q9RRU3	Q9RRU3 deinococcus
31	99.5	6.0	1056	2 Q8A7L7	Q8A7L7 bacteroides

32	99.5	6.0	1500	2 Q9BKH1	Q9BKH1 drosophila
33	99	6.0	732	2 Q6ZB62	Q6ZB62 synechocyst
34	99	6.0	794	2 Q7WZD3	Q7WZD3 bartonella
35	99	6.0	917	1 SLAP_THETH	P35830 thermus the
36	98.5	6.0	615	2 Q8J0Y2	Q8J0Y2 cryptococcu
37	98.5	6.0	883	2 Q9S526	Q9S526 drosophila
38	98.5	6.0	1500	2 Q9V4C8	Q9V4C8 drosophila
39	98	6.0	612	2 Q52903	Q52903 citrobacter
40	98	6.0	1175	2 Q8RHT3	Q8RHT3 fusobacteri
41	98	6.0	3711	2 Q6FDW3	Q6FDW3 actinobact
42	97.5	5.9	443	2 Q890Y8	Q890Y8 clostridium
43	97.5	5.9	684	1 FLID_HELPY	P96786 helicobacte
44	97.5	5.9	1507	2 Q6WIA0	Q6WIA0 bdellovibri
45	97.5	5.9	2363	2 Q6ALH2	Q6ALH2 desulfotale

ALIGNMENTS

RESULT 1					
ID	Q9X6P2	PRELIMINARY;	PRT;	320 AA.	
AC	Q9X6P2;				
DT	01-NOV-1999 (TRMBLrel. 12, Created)				
DT	01-NOV-1999 (TRMBLrel. 12, Last sequence update)				
DT	01-MAR-2004 (TRMBLrel. 26, Last annotation update)				
DE	Adhesin MafA.				
GN	Name=mafA;				
OS	Neisseria gonorrhoeae.				
OC	Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;				
OC	Neisseriaceae; Neisseria.				
OX	NCBI_TaxID=485;				
RN	(1)				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=MS11;				
RA	Eickertjaeger S., Meyer T.F., Fischer E., Maier J., Manning P.A.,				
RA	Rudel T., Scheuerpflug I., Schulz E., Schwan E.T.;				
RL	Submitted (Apr-1999) to the EMBL/Genbank/DBJ databases.				
DR	EMBL, AF142582; AAD3038.1; ..				
SQ	SEQUENCE 320 AA; 34779 MW; EE37DEC55E27DCE3 CRC64;				
Query Match					
Best Local Similarity 100.0%; Pred. No. 5.1e-125; Length 320;					
Matches 320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
QY	1	MRARLLIPILFSLVFLSACGTLTGIPSHGGKRFVDEGLVAASARAANKMDLALHGR	60		
DB	1	MRARLLIPILFSLVFLSACGTLTGIPSHGGKRFVDEGLVAASARAANKMDLALHGR	60		
QY	61	KVALYIATMGOGSGSLTGRYSIDALRGEYINSPARTDVTYRYETTAETTSGLTGG	120		
DB	61	KVALYIATMGOGSGSLTGRYSIDALRGEYINSPARTDVTYRYETTAETTSGLTGG	120		
QY	121	LTTSLSTINAPALSTRQDSGSRSSLGINIGMGDYNNETLTTPRDTAFSLHVGTVF	180		
DB	121	LTTSLSTINAPALSTRQDSGSRSSLGINIGMGDYNNETLTTPRDTAFSLHVGTVF	180		
QY	181	FLRGIDVVS PANADTVFINIDVFCTINRTEMLYNAETLKAQTKLEYFAVDRTNKKLL	240		
DB	181	FLRGIDVVS PANADTVFINIDVFCTINRTEMLYNAETLKAQTKLEYFAVDRTNKKLL	240		
QY	241	IKPKTNAFEAYKENVALMGPKYKSKIKPREGIMVDSPIRPGNHTGNSAPSEVADN	300		
DB	241	IKPKTNAFEAYKENVALMGPKYKSKIKPREGIMVDSPIRPGNHTGNSAPSEVADN	300		
QY	301	SHEGYGSDAIVRHRQGP 320			
DB	301	SHEGYGSDAIVRHRQGP 320			
RESULT 2					
ID	Q9JWK7	PRELIMINARY;	PRT;	320 AA.	

AC Q9JWK7; (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
 DE Adhesin.
 GN Name=mafa; OrderedLocustNames=NMA0325;
 OS Neisseria meningitidis (serogroup A).
 OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
 OC Neisseriaceae; Neisseria.
 NCBI_TaxID=65699;
 RX STRAIN=Z2491 / Serogroup A / Serotype 4A;
 RX MEDLINE=20222556; PubMed=10761919; DOI=10.1038/35006655;
 RA Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C.M.,
 RA Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T.,
 RA Davies K.M., Davis P., Devlin K., Feltham T., Hamlin N., Holroyd S.,
 RA Jørgensen K., Leather S., Mouton S., Mungall K.L., Quail M.A.,
 RA Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J.,
 RA Whitehead S., Spratt B.G., Barrell B.G.;
 RT "Complete DNA sequence of a serogroup A strain of Neisseria
 meningitidis Z2491".
 RL Nature 404:502-506(2000).
 DR EMBL; AL162752; CAB83630.1; -.
 DR PIR; C82028; C82028.
 KW Complete proteome.
 SQ SEQUENCE 320 AA; 34753 MW; C45EBBA8EECDE49 CRC64;

Query Match 98.7%; Score 1624; DB 2; Length 320;
 Best Local Similarity 98.4%; Pred. No. 2,5e-123;
 Matches 315; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

OY 1 MRARLLITLPSVFILSACGTLTGIPSHGGGRFAVEOELVAASARAAMKMDLQALHGR 60
 DB 1 M0ARLLITLPSVFILSACGTLTGIPSHGGGRFAVEOELVAASARAAMKMDLQALHGR 60
 OY 61 KVALYIATMGDGGSGSLTGRYSIDALI RGEYINSPAVRTDYTYRYETTAETTSGLTJG 120
 DB 61 KVALYIATMGDGGSGSLTGRYSIDALI RGEYINSPAVRTDYTYRYETTAETTSGLTJG 120
 OY 121 LTTSTLNAPALSTQSDGSGSRSLGINTGMDYNETLTNPRTAFLSHVQTVF 180
 DB 121 LTTSTLNAPALSTQSDGSGSRSLGINTGMDYNETLTNPRTAFLSHVQTVF 180
 OY 181 FLRGIDVSPNADTVFINIDVFGTINRTETMELYNATLKAOTKLEYFADVTRNKLL 240
 DB 181 FLRGIDVSPNADTVFINIDVFGTINRTETMELYNATLKAOTKLEYFADVTRNKLL 240
 OY 241 IKPKTNAFEAAVKENYALMGPYKVKSGIKPTGIMVDFSDIRPYGNHTGNSAPSEADN 300
 DB 241 IKPKTNAFEAAVKENYALMGPYKVKSGIKPTGIMVDFSDIRPYGNHTGNSAPSEADN 300
 OY 301 SHEGYSDEAVRHRGQOP 320
 DB 301 SHEGYSDEAVRHRGQOP 320
 RESULT 3
 O9JWS4 PRELIMINARY; PRT; 313 AA.
 AC Q9JWS4;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 25-OCT-2004 (TREMBLrel. 26, Last annotation update)
 DE MafA protein.
 GN OrderedLocustNames=NMB0375, NMB0652;
 OS Neisseria meningitidis (serogroup B).
 OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
 OC Neisseriaceae; Neisseria.
 NCBI_TaxID=491;
 RX STRAIN=MCS8 / Serogroup B;
 RX MEDLINE=20175755; PubMed=10710307; DOI=10.1126/science.287.5459.1809;
 RA Tetrelin H., Saunders N.J., Heidelberg J.F., Jeffries A.C.,
 RA Nelson K.E., Eisen J.A., Ketchum K.A., Hood D.W., Peden J.C.,
 RA Dodson R.J., Nelson W.C., Gwinn M.L., DeBoy R.T., Peterson J.D.,
 RA Hickey E.K., Hatt D.H., Salzberg S.L., White O., Fleischmann R.D.,
 RA Dougherty B.A., Mason T.M., Ciecko A., Parksey D.S., Blair B.,
 RA Citron G.H., Clark E.B., Cotton M.D., Uterback T.R., Khouri H.M.,
 RA Qin H., Vamathevan J.J., Gill J., Scarlato V., Maignan V., Piza M.,
 RA Grandi G., Sun L., Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R.,
 RA Venter J.C.;
 RT "Complete genome sequence of Neisseria meningitidis serogroup B strain
 MCS8".
 RL Science 287:1809-1815(2000).
 DR EMBL; AE002393; AAF62309.1; -.
 DR EMBL; AE002420; AAF41073.1; -.
 DR PIR; G81173; G81173.
 DR TIGR; NMB0375; -.
 DR TIGR; NMB0652; -.
 KW Complete proteome.
 SQ SEQUENCE 313 AA; 34000 MW; 360676272DAD60C1 CRC64;

Query Match 62.6%; Score 1029; DB 2; Length 313;
 Best Local Similarity 62.7%; Pred. No. 4.3e-75;
 Matches 197; Conservative 49; Mismatches 62; Indels 6; Gaps 2;

OY 5 LLIPILPSVFILSACGTLTGIPSHGGGRFAVEOELVAASARAAMKMDLQALHGRKVAL 64
 DB 6 LLIPL-----VLTACGTLTGIPSHGGGRFAVEOELVAASARAAMKMDLQALHGRKVAL 60
 OY 65 YIATMGDGGSGSLTGRYSIDALI RGEYINSPAVRTDYTYRYETTAETTSGLTJG 124
 DB 61 YVSWMGDGGSGSLTGRYSIDALI RGEYINSPAVRTDYTYRYETTAETTSGLTJG 120
 OY 125 LSTLNAPALSTQSDGSGSRSLGINTGMDYNETLTNPRTAFLSHVQTVF 184
 DB 121 TSLNAPALATKNSGKGRSAGLSVNGDYNELTNPRTAFLSHVQTVF 180
 OY 185 IDVSPNADTVFINIDVFGTINRTETMELYNATLKAOTKLEYFADVTRNKLL 244
 DB 181 IEVPEPADTVFINIDVFGTINRTETMELYNATLKAOTKLEYFADVTRNKLL 240
 OY 245 TNAFEAAVKENYALMGPYKVKSGIKPTGIMVDFSDIRPYGNHTGNSAPSEADN 304
 DB 241 TAAEYQYOEQYALMTGPYKVKSKVAKSDRLMDFSDITPYGTTAQRNPDPKONGK 300
 OY 305 YGVSDEAVRHRGQOP 318
 DB 301 -DVGNEVIRRRKGG 313
 RESULT 4
 O9JWS0 PRELIMINARY; PRT; 313 AA.
 AC Q9JWS0;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
 DE Adhesin MafA2.
 GN Name=mafa2; OrderedLocustNames=NMA2112;
 OS Neisseria meningitidis (serogroup A).
 OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
 OC Neisseriaceae; Neisseria.
 NCBI_TaxID=65699;
 RX STRAIN=Z2491 / Serogroup A / Serotype 4A;
 RX MEDLINE=20222556; PubMed=10761919; DOI=10.1038/35006655;
 RA Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C.M.,
 RA Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T.,
 RA Davies K.M., Davis P., Devlin K., Feltham T., Hamlin N., Holroyd S.,
 RA Jørgensen K., Leather S., Mouton S., Mungall K.L., Quail M.A.,
 RA Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J.,
 RA Whitehead S., Spratt B.G., Barrell B.G.;

RT "Complete DNA sequence of a serogroup A strain of *Neisseria meningitidis* 22481.".
RL Nature 404:502-506(2000).
DR EMBL; AL162758; CAB85326.1; -.
DR PIR; G81782; G81782.
KW Complete proteome.
SQ SEQUENCE 313 AA; 33929 MW; DF876F2C537C5D7D CRC64;

Query Match 62.4%; Score 1026; DB 2; Length 313;
Best Local Similarity 62.4%; Pred. No. 7, 5e-75;
Matches 196; Conservative 49; Mismatches 63; Indels 6; Gaps 2;

QY 5 LLIPLFLVFLISACGLTIGIPSHGGRFAVEQLVAASARAAYKMDLALHGRKVAL 64
DB 6 LLIPL-----VLIACGLTILGIPAHGGGRFAVEQLVAASARAAYKMDLSLHGRKVAL 60
QY 65 YIATMGDGGSGSLTGGRYSIDALIRGEYINSPAVRTDYTPRYETTAETTSGLTGLTTS 124
DB 61 YVSVNGDGGSGNISGGRYSIDALIRGYHNPESATQSYPAVDITATTKSDALSSVTS 120
QY 125 LSTLAPALSRQTSGSGSSRLGLNIGMGDYRNETLTNPRDTAFSLHLYQVTFPLRG 184
DB 121 TSLTAPAPALTLKNGSRKGRSAGLSVNGTGDYRNETTLANPRDVSFLTNLIQTIVFYLRG 180
QY 185 IDVSPANADTDVFINIDVFGTIRNRTMHLNNAETLKAQTKLEYFAVDRTMKLLIKPK 244
DB 181 IEVPEPYADTDVFTVDVFGTIRNRTMHLNNAETLKAQTKLEYFAVDROSRKLLIAPK 240
QY 245 TNAPFAAYKENYALMMGPKYKSKGIKPTGELMVDSDIRPYGNHTGNSAPSEADNSHEG 304
DB 241 TAAVSSQIQEOYALMMGPKYKSKGTVKASDRLMVDPSDITPYGDDTTAQNRPDKQNGKKP 300
QY 305 YGYSDEAVRQHRQG 318
DB 301 -DVGNEVIRRRKGG 313

RESULT 5

ID Q8VP63 PRELIMINARY; PRT; 511 AA.
AC Q8VP63;
DT 01-MAR-2002 (TREMBLrel. 20, Created)
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Alkaline phosphatase.
GN Name:phoA;
OS Mycobacterium smegmatis.
OC Bacteria; Actinobacteria; Actinobacteriales; Actinomycetales;
OC Corynebacteriaceae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1772;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22778081; PubMed=12897018;
RX DOI=10.1128/JB.185.16.4983-4991.2003;
RA Kriakov J. I., Lee S. H., Jacobs W. R., Jr.;
RT "Identification of a regulated alkaline phosphatase, a cell surface-associated lipoprotein, in *Mycobacterium smegmatis*."
RL J. Bacteriol. 185:4983-4991(2003).
CC -1 SIMILARITY: Belongs to the alkaline phosphatase family.
DR EMBL; AY065934; AAL50185.1; -.
DR HSSP; P06634; IAJA.
DR GO; GO:0008152; P:metabolism; IEA.
DR Pfam; PF00245; Alk_phosphatase; 1.
DR PRINTS; PR00113; ALKPHPTASE.
DR SMART; SM00098; alkPc; 1.
DR PROSITE; PS00123; ALKALINE_PHOSPHATASE; 1.
SQ SEQUENCE 511 AA; 53697 MW; FCB27A3A561C92C CRC64;

Query Match 7.4%; Score 122.5; DB 2; Length 511;
Best Local Similarity 21.7%; Pred. No. 0.26;
Matches 75; Conservative 41; Mismatches 105; Indels 135; Gaps 17;
QY 1 MRARLLILRSVFLISACGLTIGIPSHGGRFAVEQLVAASARAAY-----KMDLQA 56

DB 7 LRATVIV-VAALALPLTCCSSDITTESSGDIYHNSADDITNGCARIDGQDITERSA 65
QY 57 LHGRKVALYIATMGD-QGSGSLT-----GGRY-SIDAL-IRGEYINSPAVRTDYTY 104
DB 66 INGGKARNVILLVGDGMDSEITMARNYEKAGGSGFDLADLPLSGQY-----TLYAL 118
QY 105 -----PRYETTAETTSGLTGLTSLTNLP-----ALSRQSDGSG----- 142
DB 119 NKDGKPNVTVTSASA--TGMVTGTYKYNALGIDKGNPQKTLLELAKQGFATGDTV 175
QY 143 -----SRSSL-----GLNIGMGDYRNETLTNPRDTAFSL 173
DB 176 TSEIADATASALFHSISRDCYQVQTADCAADALEGSGSYTEQLITRP----- 228
QY 174 HLVOVTFPLRGIDVSPANADTDVFINIDVFGTIRNRTMHLNNAETLKAQTKLEYPAVD 233
DB 229 -----DLTLGGAEY-----FSQTNAGE-----YKQKTLLEAQAKERGFOIV 265
QY 234 RTNKKLLIKPTNAFEAYKENYAL-----MMGPKYKSKG 268
DB 266 RTASL-----DAVTADQDNPVYGLFADGNMPVMSGPPAVRHG 305

RESULT 6

ID Q6NP01 PRELIMINARY; PRT; 729 AA.
AC Q6NP01;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE H104242P (Fragment).
GN Name:rdgB;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkley;
RA Stapleton M., Brokstein P., Hong L., Aspayani A., Carlson J.,
RA Champagne M., Chavez C., Dorsett V., Dresnek D., Farfan D., Friese E.,
RA George R., Gonzalez M., Guarin H., Krommiller B., Li P., Liso G.,
RA Miranda A., Mungall C.D., Nunoo J., Paclebe J., Paragae V., Park S.,
RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
RA Ceiniker S.;
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BT011130; AAR82797.1; -.
DR GO; GO:0046872; P:metal ion binding; IEA.
DR InterPro; IPR004177; DDHD.
DR Pfam; PF02862; DDHD; 1.
FT NON TER 1
SQ SEQUENCE 729 AA; 79585 MW; 355F7B37BAE3A995 CRC64;

Query Match 7.1%; Score 117.5; DB 2; Length 729;
Best Local Similarity 23.7%; Pred. No. 1;
Matches 82; Conservative 39; Mismatches 106; Indels 119; Gaps 18;

QY 14 FILSACGLTIGIPSHGGR-----KFAVEQLVAASARA-----AYKD 51
DB 394 FILRQIGKEFEGIPFGVSGDDKDNASFHRCGRREKKIKRTSVKLKNVAANRAVDVIOE 453
QY 52 -----MDLQALHGRKVALYIATMGDGGSGSLT-----GGR--YSID- 85
DB 454 GREORLNARFMYGGLMDITLGEKVDVHI--MKDPPAGEWTFLESTVTDKNGRISYSIPD 511
QY 86 --ALIRGEYINSPAVRTDYTY-----PRYETTAETTSGLTGLTSLTSL-TLNAPAL 133
DB 512 QVSLGYGYIPKMYKRGDHTSVDCYMAVVPFLTECVPSIDG---SFLASNSVGRDPKV 568
QY 134 SRTQSDGSGSSRLG--LNLIGMGDYRNET-----LTTNP--RD 168

Db 569 RAGAVDVCRRHQEGLYLLIYITGRPDMQOQRVSWLSQHNPHGLISFADGLSTDPGLGHK 628
Qy 169 TAPLSHVQTVFFLRGIDVVS PANADTVFINIDVFGTIRNRTEMLHYNMTELLAQKTKLE 228
Db 629 TAYLNNLVQN---HGSIITAAVSSKD---ISVYINVGKRTD-----Q 665
Qy 229 YFAVDRTNKULLIKPTNAFEAAKENYALMGPYKYSKGIKPTG 274
Db 666 IFIVGKVGKTL---QSNV---TVLSDGYAAHLGLAQVGSRPAGK 705

RESULT 7
002434 PRELIMINARY; PRT; 1250 AA.
AC 002434;
DT 01-JUN-1997 (TREMBlrel. 04, Created)
DT 01-JUL-1997 (TREMBlrel. 04, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Retinal degeneration B protein.
GN Name=rdgB;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OC NCBI_TaxId=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Oregon-R; TISSUE=Head;
RX MEDLINE=91231170; PubMed=1903119;
RA Vithelic T.S., Hyde D.R., O'Tousa J.E.,
RT "Isolation and characterization of the Drosophila retinal degeneration
B (rdgB) gene."
RL Genetics 127:761-768(1991).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Oregon-R; TISSUE=Head;
RX MEDLINE=98343889; PubMed=9680295;
RA Rubboli F., Bulfone A., Bogni S., Marchitelli A., Zolli M.,
RA Porsani G., Ballabio A., Banfi S.,
RT "A mammalian homologue of the Drosophila retinal degeneration B gene:
implications for the evolution of phototransduction mechanisms."
RL Genes Funct. 1:205-213(1997).
DR HSBP; Y08035; CAA69291.1; -.
DR FLYBase; FBgn0003218; rdgB.
DR GO; GO:0016021; C:integral to membrane; TAS.
DR GO; GO:0016029; C:subrhabdomeral cisterna; NAS.
DR GO; GO:0008525; F:phosphatidylcholine transporter activity; IDA.
DR GO; GO:0008526; F:phosphatidylinositol transporter activity; IDA.
DR GO; GO:0016059; P:deactivation of rhodopsin mediated signaling; IMP.
DR GO; GO:0007608; P:perception of smell; IMP.
DR GO; GO:0016052; P:phototransduction; TAS.
DR GO; GO:0016056; P:rhodopsin mediated signaling; IMP.
DR InterPro; IPR004177; DDHD.
DR InterPro; IPR018662; P1_transfer.
DR Pfam; PF02121; IP_trans; 1.
DR PRINTS; PR00391; FITRANSFER.
SQ SEQUENCE 1250 AA; 137777 MW; 3CC926ABBA0A6F28 CRC64;

Query Match 7.1%; Score 117.5; DB 2; Length 1250;
Best Local Similarity 23.7%; Pred. No. 2.1;
Matches 82; Conservative 39; Mismatches 106; Indels 119; Gaps 18;

Qy 14 FILSACCTGTCIRPHGGG-----KRPVDEELVAASARA---AVKD 51
Db 906 FILRQIKFESGIFPVGSNDKDNASFPHGQRPREWKIKRISVKLVAAANRRADVIVQE 965
Qy 52 -----MDQLALHGRKVALYIATMGDQSGSLT-----GGR--YSID- 85
Db 966 GREORLWARRFMYGGLDMITLHGEKVDAHI--MKRPAPGQWFELSTVTDKNGRISYSIPD 1023
Qy 86 --ALIRGEYINSPAVRTDYTY-----PRYETIAETTSGLTGLTSLIS-TLNAPAL 133

Db 1024 QVSLGYGIYFVKMVRDSDHTSVDCYMAVPEPLRECVFVSIDG---SFTASMSVGRDPKV 1080
Qy 134 SRQSDSGSRSSLSG---LNIIGMGDYRNFT-----LTTNP--RD 168
Db 1081 RAGAVDVCRRHQEGLYLLIYITGRPDMQOQRVSWLSQHNPHGLISFADGLSTDPGLGHK 1140
Qy 169 TAPLSHVQTVFFLRGIDVVS PANADTVFINIDVFGTIRNRTEMLHYNMTELLAQKTKLE 228
Db 1141 TAYLNNLVQN---HGSIITAAVSSKD---ISVYINVGKRTD-----Q 1177
Qy 229 YFAVDRTNKULLIKPTNAFEAAKENYALMGPYKYSKGIKPTG 274
Db 1178 IFIVGKVGKTL---QSNV---TVLSDGYAAHLGLAQVGSRPAGK 1217

RESULT 8
09VY88 PRELIMINARY; PRT; 1250 AA.
AC 09VY88;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE CG1111-PB.
GN Name=rdgB; ORFNames=CG11111;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OC NCBI_TaxId=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20196006; PubMed=10711132; DOI=10.1126/science.287.5461.2185;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Mandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.H., Blazer R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabot G.L.,
RA Abrial J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Botkova D., Botchan M.R., Bouck J., Brokstein P., Brotlier P.,
RA Burtis K.C., Buzam D.A., Butler H., Cadiou E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriere S., Fleischmann W.,
RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwan C.,
RA Jaitai M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Laeko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang X., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacלב J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Sanders R.D., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spler E., Spradling A.C., Stapleton M., Strong R., Sun B.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.Y., Wasserman D.A., Weisbrock G.M., Weissenbach J.,
RA Williams S.M., Woodgett, Zhan M., Zhang G., Zhu D., Yang S., Yao Q.A., Ye J.,
RA Yeh R.F., Zaveri U.S., Zhan M., Zhang G., Zhu Q., Zheng L., Zheng X.H.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster";
RL Science 287:2185-2195(2000).
RN [2]
RP SEQUENCE FROM N.A.

RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Githbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
RT "The genome sequence of *Drosophila melanogaster*,"
RL Science 287:2185-2195 (2000).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=22426065; PubMed=12537568;
RA Celniker S.E., Wheeler D.A., Krommiller B., Carlson J.W., Halpern A.,
RA Patel S., Adams M., Champe M., Dugan S.P., Fries E., Hodgson A.,
RA George R.A., Hoskins R.A., Laverly T., Muzny D.M., Nelson C.R.,
RA Paciel J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
RA Svirskaas R., Taber P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
RA Weinstein G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.,
RT "Finishing a whole-genome shotgun: Release 3 of the *Drosophila*
RT *melanogaster* euchromatic genome sequence,"
RL Genome Biol. 3:RESEARCH0079-RESEARCH0079 (2002).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=22426070; PubMed=12537573;
RA Kankiner J.S., Bergman C.M., Krommiller B., Carlson J., Svirskaas R.,
RA Patel S., Fries E., Wheeler D.A., Lewis S.E., Rubin G.M.,
RA Ashburner M., Celniker S.E.,
RT "The transposable elements of the *Drosophila melanogaster* euchromatin:
RT a genomic perspective,"
RL Genome Biol. 3:RESEARCH0084-RESEARCH0084 (2002).
RN [5]
RP SEQUENCE FROM N.A.
RX MEDLINE=22426069; PubMed=12537572;
RA Maira S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA Hradecky P., Huang Y., Kankiner J.S., Millburn G.H., Prochuk S.E.,
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
RA Bellenkourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
RA Harteis N.L., Richter J., Russo S., Schroeder A.J., Shu S.O.,
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA Lewis S.E.,
RT "Annotation of the *Drosophila melanogaster* euchromatic genome: a
RT systematic review,"
RL Genome Biol. 3:RESEARCH0083-RESEARCH0083 (2002).
RN [6]
RP SEQUENCE FROM N.A.
RG FLYBASE;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
RN [7]
RP SEQUENCE FROM N.A.
RG FLYBASE;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY051422; AAK92846.1; -;
DR EMBL; AE003493; AAF48316.2; -;
DR HSSP; P53810; IKCM.
DR FLYBASE; FBgn0003218; rdsB.
DR GO; GO:0016021; C:integral to membrane; TAS.
DR GO; GO:0016029; C:subrhabdomeral cisterna; NAS.
DR GO; GO:0008525; F:phosphatidylcholine transporter activity; IDA.
DR GO; GO:0008526; F:phosphatidylinositol transporter activity; IDA.
DR GO; GO:0016059; P:deactivation of rhodopsin mediated signaling; IMP.
DR GO; GO:0007608; P:perception of smell; IMP.
DR GO; GO:0007602; P:phototransduction; TAS.
DR GO; GO:0016056; P:rhodopsin mediated signaling; IMP.
DR InterPro; IPR004177; DDHD.
DR InterPro; IPR001666; P1_transfer.
DR Pfam; PF02862; DDHD; 1.
DR Pfam; PF02121; IP_trans; 1.
DR PRINTS; PR00391; PIRTRANSFER.
SO SEQUENCE 1259 AA; 138894 MW; 9DD40B76EB1079F7 CRC64;

Query Match 7.1%; Score 117.5; DB 2; Length 1259;
Best Local Similarity 23.7%; Pred. No. 2.2;
Matches 82; Conservative 39; Mismatches 106; Indels 119; Gaps 18;

QY 14 FILSACGTLGIPRHGG-----RRFAVEQELVASARA---AKD 51
DB 906 FILRQIGKFGESIPVGSNDKDNASFHQPGRPKWIKRTISKLVANRHRADVIVQE 965

OY 52 -----MDLQALHGRKVALYIATMGDSGSLT-----GGR--YSID- 85
DB 966 GREORLNARFMYGLDMITLHGERVDVHI--MKRPPAGEWTFLESTVWDKXGRISYSIPD 1023
OY 86 --ALIRGEYINSAPVRDITY-----PRVETTAETTSGLTGLTSLTSL--TLNAPAL 133
DB 1024 QVSLGYGYIPVGMVVRGDHTSVDCYMAVPEPLTECVFISIDG---SFTASMSVGRDPKV 1080
OY 134 SRTSGDSGSSSSIG---LIMGSGDYRNET-----LTTNP--RD 168
DB 1081 RAGAVDVCRRHMOELGYLLITYTGPRDQOCQVSMISOHNPFGHLSIFADGLSTDPGLGHK 1140
OY 169 TAPLSHVQYVFFLRGIDVVSSPANADYFINIDVFGTIRNRTEMLYNAAETLAKQTLK 228
DB 1141 TAYLNLVQN---HGSIITAAGSSND---ISVYTNVGRKD-----Q 1177
OY 229 YFVAVDRNKKLLIKPKTNAFEAAKYENYALMGPKYKSKIKPREG 274
DB 1178 IFIVGKVGKKL-----QSNNA--TVLSDGYAAHLAQLQAVGSGRPAPKG 1217

RESULT 10
OY 08KG07 PRELIMINARY; PRT; 627 AA.
AC 08KG07;
DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Alpha oxoglutarate ferredoxin oxidoreductase, alpha subunit.
GN OrderedLocustNames=CT0163;
OS Chlorobium tepidum.
OC Bacteria; Chlorobi; Chlorobia; Chlorobiales; Chlorobiaceae;
CX NCBI_TaxID=1097;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=TLS / ATCC 49652 / DSM 12025;
RX MEDLINE=22103685; PubMed=12093901; DOI=10.1073/pnas.132181499;
RA Eisen J.A., Nelson K.E., Paulsen I.T., Heidelberg J.F., Wu M.,
RA Dodson R.J., DeBoy R.T., Gwinn M.L., Nelson W.C., Haft D.H.,
RA Hickey E.K., Peterson J.D., Durkin A.S., Kolonay J.F., Yang F.,
RA Holt I.E., Umayam L.A., Mason T.M., Brenner M., Shea T.P.,
RA Parksey D.S., Niernan W.C., Feldblyum T.V., Hansen C.L., Craven M.B.,
RA Radune D., Vamathevan J.J., Khouli H.M., White O., Gruber T.M.,
RA Ketchum K.A., Venter J.C., Tettelin H., Bryant D.A., Fraser C.M.,
RT "The complete genome sequence of *Chlorobium tepidum* TLS, a
RT photosynthetic, anaerobic, green-sulfur bacterium,"
RL Proc. Natl. Acad. Sci. U.S.A. 99:9509-9514 (2002).
DR EMBL; AE012796; AAM71411.1; -;
DR TIGR; CT0163; -;
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR002869; POR.
DR InterPro; IPR009014; Transketo_C_like.
DR Pfam; PF01558; POR; 1.
KV Complete proteome.
SO SEQUENCE 627 AA; 67379 MW; 4483729463DA2BA4 CRC64;

Query Match 7.0%; Score 114.5; DB 2; Length 627;
Best Local Similarity 21.6%; Pred. No. 1.5;
Matches 61; Conservative 40; Mismatches 93; Indels 89; Gaps 12;

OY 61 KVALYIATMGDSG--SLTGRYSIDLIRGEYINSAPVRTDYTPRYETTAETTSGLT 119
DB 16 KTNVSVLPFADSGSGGMQLTGQFANVAVGSDLN-----TFPNPSSIRRPAGVVA 67
OY 120 GL-----TTSLSI-----LNAPLSR-----TQSDGSGSSSLGL 149
DB 68 GVSGFQLOFGTGYTGCAKFDVMIAMNAAALKANLKHGGIITADTGFDAKN--L 124
OY 150 NIGGMDYRNETLTTPRDPAFLSHVQYVFFLRGIDVVSSPANADT-----DVFINID 202

Db 125 NLAGYGE-----TNNPLEDGTLD--YTFVKIPVLSLRLQALADTGLSTKIIDRCXNMF 176
Qy 203 VFGTIRNRTTMLLYNAETLKAKOTKLEYPFVNDRTNKKLIKPKTNAFEAY-----K 253
Db 177 VLGV-----LYWLYSLPLETTIEALQSKFKKNQDIAENAIKAVKAGYNFGDETEMFS 228
Qy 254 ENYALMGPYKYSKGIKPTGGLMVPFSDIRPYGNHTGNSAPSY 296
Db 229 OHGRECVPPAQKKGV-----YRRVTGNBSAI 256

RESULT 11

08XSD6 PRELIMINARY: PRT: 3552 AA.
ID 08XSD6
AC 08XSD6
DT 01-MAR-2002 (TREMBLrel. 20, Created)
DT 01-MAR-2002 (TREMBLrel. 20, last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, last annotation update)
DE PROBABLE HEMAGGLUTININ-RELATED PROTEIN.
CN Name=RS05701; OrderedLocustNames=RS0540;
OS Ralstonia solanacearum (Pseudomonas solanacearum).
OC Plasmid megaplasmid.
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Burkholderiaceae; Ralstonia.
OX NCBI_TaxId=305;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GM1100;
RX MEDLINE=21681879; PubMed=11823852; DOI=10.1038/415497a;
RA Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S.,
RA Arlat M., Billault A., Brotier P., Camus J.C., Cartolico L.,
RA Chandler M., Choise N., Claudel-Bernard C., Cunac S., Demange N.,
RA Gaopin C., Lavie M., Moisan A., Robert C., Saurin W., Schlex T.,
RA Sigler P., Theubalt P., Whalen M., Winkler P., Levy M.,
RA Weissbach J., Boucher C.A.;
RT "Genome sequence of the plant pathogen Ralstonia solanacearum";
RL Nature 415:497-502(2002).
DR EMBL; AL646079; CAD17691.1; -;
DR Pfam; PF05594; Fil_haemag; 21.
DR Pfam; PF05860; Haemag_act; 1.
DR SMART; SM00710; PBH1; 6.
DR TIGRFAMs; TIGR01901; adhe_NPKG; 1.
DR TIGRFAMs; TIGR01731; fil_hemag_20aa; 15.
DR PROSITE; PS01070; NUCLEASE_NON_SPEC; UNKNOWN_1.
KW Complete proteome; Plasmid.
SQ SEQUENCE 3552 AA; 352934 MW; C5432AABE2CCF59C CRC64;

Query Match 6.8%; Score 111.5; DB 2; Length 3552;
Best Local Similarity 20.0%; Pred. No. 26;
Matches 84; Conservative 51; Mismatches 141; Indels 145; Gaps 17;

Qy 16 LSAAGTLT-----GIPSHGGKRAVEQELVAASARAAYKMDLQALHGRVALYIATM 69
Db 998 LSAANNLTLDGSGAVINQSGMRGAVSLNNAIDNTSGKIGNDAGSGSVAMTTGSL 1057
Qy 70 GDGSG-----SLTGRYSIDA-----LIRGEYNPAVRIDYTPRETTAE 112
Db 1058 ANOGGAISDRNLSTTGLSDGRIIAGDGCAITINGTYSANQIOAN-----NLTL 1113
Qy 113 TTSGLTGLTSLSTLNAALSRQSDGSG-----SRSLGLNIG-----MGDYRNETLTT 164
Db 1114 TTTGLTNGCT-LAAVNLTVAAVNDNAGADLMSASISVAGAGAITMAGIIBDDYTT 1172
Qy 165 -----NPRDTAFLSHLV-----TFPFLKGI 185
Db 1173 OSGAFANTGVGNVNTLNAGAIISYTGASAPALAAATQNLVASDRLSNTGATLPSLGI 1232
Qy 186 DVVSPANADTVFINIDVGTIRNRTTMLLYNAETLKAKOTKLEYP--AYDRNKKLLIKP 243
Db 1233 NIAANGARDN-----GLANRSNLTNDOSTIEAGNLEIATQTLNTRPEPTYOT 1284
Qy 244 KTNAAEAYKE-----NYALMGPYKV-----SKGK 270

Db 1285 VTTGTSTAHETRKGYACATWMAAPHGCGCTQAVWNNSGYKTPIDATFTPTAQIVSQTSGBN 1344
Qy 271 PTEGLMV-----DESDIRPYGN-----HNGNAPSYE---ADNSHSG 304
Db 1345 PVDNYLVVWNGQNTIYVNAVNTNGNGTIVVYDADPH--NVVPSYEVATRSRGHG 1403
Qy 305 Y 305
Db 1404 Y 1404

RESULT 12

06G428 PRELIMINARY: PRT: 874 AA.
ID 06G428
AC 06G428
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, last annotation update)
DE Hypothetical protein.
CN OrderedLocustNames=BH05510;
OS Bartonella henselae (Rochalimaea henselae).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Bartonellaceae; Bartonella.
OX NCBI_TaxId=38323;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 49882 / Houston 1;
RX PubMed=15210978; DOI=10.1073/pnas.0305659101;
RA Alenmark U.C.M., Frank A.C., Karlberg E.O., Legault B.-A., Ardeli D.H.,
RA Candaeck B., Eriksson A.-S., Naeslund A.K., Handley S.A., Huvel M.,
RA La Scola B., Holmberg M., Andersson S.G.E.;
RT "The house-borne human pathogen Bartonella quintana is a genomic
derivative of the zoonotic agent Bartonella henselae";
RL Proc. Natl. Acad. Sci. U.S.A. 101:9716-9721(2004).
DR EMBL; BX897699; CAF27359.1; -;
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR006315; Autotransporter.
DR InterPro; IPR005546; Auto_transbeta.
DR InterPro; IPR011050; Pectin_lyas_like.
DR InterPro; IPR004899; Pectactin.
DR InterPro; IPR003991; Pectactin_C.
DR Pfam; PF03797; Autotransporter; 1.
DR Pfam; PF03212; Pectactin; 1.
DR PRINTS; PR01484; PRTACTNFMALY.
DR TIGRFAMs; TIGR01414; autotrans_barl; 1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 874 AA; 95156 MW; 705381D8B17C958B CRC64;

Query Match 6.6%; Score 109; DB 2; Length 874;
Best Local Similarity 19.9%; Pred. No. 6.5;
Matches 65; Conservative 52; Mismatches 125; Indels 84; Gaps 13;

Qy 11 FSVFILSAC-----GTLGIPSHGG-GKRAVEQELVAASARAAYKMDL 54
Db 9 FSVFILSCFQVVASASENKRALKKITSVTSGGKIAKSSALVTGSLIPSSNIMIQDGV 68
Qy 55 QALHGRKALYIATMGDGGSLTGRYSIDLIG-----ETINPAVATDTPRYETT 110
Db 69 EIVENGKTSIG-ATVEEGKQIVTRGKAIDIKRIGGQKQFVEESPANFD--LORQSSA 125
Qy 111 AETSGGLTGLTSLSTL-NAPALSRQSDGSGRSSLGLNIGMGDYNETLTTNPRDT 169
Db 126 YDAIVSGNGVGGQNVYDDAKAMNTYKTQGGSEQNLKYNKKRIGGFANTVVSNGRGH 185
Qy 170 AFLSHL-VQVFEFLGIDVSP-----ANADTVFINIDVGTIRNRTTMLLYNA 218
Db 186 ILAEGMATNTILKDAVQVVFYGGIIDLTVNGSASSMLYVAGADLQGEIKVNDKGLY-- 243
Qy 219 ETLKAKOTKLEYPFVNDRTNKKLIKPKTNAFEAYKENVALMGPYKYSKGIKPTG 274
Db 244 -----LPAGRTHIIRKLFVEGRV-----AEWL-----FGV----- 271
Qy 275 LMVDFSDIRPYGNHTGNSAPVEADN 300

Db 272 -----GERNNETPOLEIDS 286

RESULT 13

06BCF8 PRELIMINARY; PRT; 684 AA.

AC 06BCF8: 25-OCT-2004 (TREMBlrel. 28, Created)
 DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)
 DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)
 DE Chitinase A.
 GN Name=Chia;
 OS Lyso bacter enzymes.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
 OC Xanthomonadaceae; Lyso bacter.
 NX NCBI_TaxID=69;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C3;
 RA Kobayashi D.Y., Reedy R.M., Bick J., Yuen G.Y.;
 RT "The chia gene encodes for major chitinase activity expressed by
 RL Lyso bacter enzymes C3.";
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Contains 1 fibronectin type III domain.
 DR EMBL: AY67480; AAT77163.1; -;
 DR GO: GO:0005576; C:extracellular; IEA.
 DR GO: GO:0030246; F:carbohydrate binding; IEA.
 DR GO: GO:0016787; F:hydrolase activity; IEA.
 DR GO: GO:0004553; F:hydrolase activity; hydrolyzing O-glycosyl . . ; IEA.
 DR GO: GO:0005975; P:carbohydrate metabolism; IEA.
 DR GO: GO:0008152; P:metabolism; IEA.
 DR InterPro: IPR003610; CEM_5_12;
 DR InterPro: IPR011583; Chitinase II.
 DR InterPro: IPR003962; FmII subd.
 DR InterPro: IPR003961; Fm_III.
 DR InterPro: IPR008957; Fm_III-like.
 DR InterPro: IPR001223; Glyco_hydro_18.
 DR InterPro: IPR001579; Glyco_hydro_18AS.
 DR Pfam: PF02839; CEM_5_12; 1.
 DR Pfam: PF00041; Fm3; 1.
 DR Pfam: PF00704; Glyco_hydro_18; 1.
 DR PRINTS: PR00014; FNTYPEIII.
 DR ProDom: PD000471; Chitinase_II; 1.
 DR SMART: SM00060; Fm3; 1.
 DR SMART: SM00636; Glyco_18; 1.
 DR PROSITE: PS01095; CHITINASE_18; 1.
 DR PROSITE: PS00853; Fm3; 1.
 DR GlycoSite: Hydrolase.
 SQ SEQUENCE 684 AA; 71453 MW; D54ECF589E9E15E CRC64;

Query Match 6.5%; Score 107; DB 2; Length 684;

Best Local Similarity 26.1%; Pred. No. 6.8;

Matches 54; Conservative 25; Mismatches 84; Indels 44; Gaps 10;

QY 16 LSAGCTLTG-----IPSHGGKRPVAGQELVAAARAAYVQMDLQALHGK--VAL 64
 DB 78 LGVCTGTEGNOPTVSLTAPNSGATYNAGAN---IAVSANAAADSDGASVAFRRGTTSL 134
 QY 65 YIATMGDGS--GSLTGGYSIDALIRGEYINSPAVRTDYTYPRYETTAETTSGLT--- 119
 DB 135 GVDTSAPYGVMTNATAGNHSFTAVAKD---NQNAATTS-----SAVAATVVGSSSDTT 185
 QY 120 -----GTTTSLSTLNAPALS-RTOSDGSGRSSISGLNIGMGDYRNETLTTPRDTAF- 171
 DB 186 PPSVPGGLASSSQPANSVLSLWNAIDMSG-----GSGVADYDYRNGSLAGSPTTTSYT 240
 QY 172 ---LSHLVQVTFPLRGIDVVS PANADT 195
 DB 241 VSGLSPTSTSYSTFVRARDNAGNASHQS 267

RESULT 14

06AVK7 PRELIMINARY; PRT; 731 AA.

AC 06AVK7: 25-OCT-2004 (TREMBlrel. 28, Created)
 DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)
 DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)
 DE Putative transcription factor.
 GN Name=OSUNBA0022C08.1;
 OS Oryza sativa (japonica cultivar-group).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzaceae; Oryza.
 NX NCBI_TaxID=39947;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Buell C.R., Yuan Q., Ouyang S., Liu J., Gansberger K., Jones K.M.,
 RA Overton II L.L., Taitlin T., Kim M.M., Bera J.J., Jin S.S.,
 RA Fadrosh D.W., Tallon L.J., Koo H., Zismann V., Hsiao J., Blunt S.,
 RA Vanaken S.S., Riedmuller S.B., Utecherback T.T., Feldblyum T.V.,
 RA Yang Q.Q., Haas B.J., Suh B.B., Peterson J.J., Quackenbush J.,
 RA White O., Salzberg S.L., Fraser C.M.;
 RT "Oryza sativa chromosome 3 BAC OSUNBA0022C08 genomic sequence."
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Buell R.;
 RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AC097277; AAT81711.1; -;
 DR InterPro: IPR005202; GRAS.
 DR InterPro: IPR009014; Transketo_C_1like.
 DR Pfam: PF03514; GRAS; 1.
 SQ SEQUENCE 731 AA; 82218 MW; D3E04E65004364D7 CRC64;

Query Match 6.4%; Score 105.5; DB 2; Length 731;

Best Local Similarity 23.2%; Pred. No. 9.8;

Matches 63; Conservative 39; Mismatches 103; Indels 66; Gaps 12;

QY 93 INSPAVRTDYTYPRYETTAETTSGLTGLTSLTNAAPALRTQSDGSGRSSISGLN-- 150
 DB 134 LDSPSESTSSYP-HSLASSTSNISGAVDS-----SQRRYVGHSHYRLSGHSS 183
 QY 151 ---TGKMGDYRN-----ETLTTPRDTAFLSHLVQVTFPLRGIDVVS PANADT-VFIN 200
 DB 184 QPVPGPSVDYRNAMETLEDPLISNGRIPEYLFESFTWDFRGRGDEAQKFLPGSDKVID 243
 QY 201 IDVFGTIRNR-----TSMHLYNAETLKAQ-----TKLEYFADV----- 233
 DB 244 LEAGVAKRQDAGKAISLWVSKAVLVKKNRQSEDLIDWEGNRSKQSAFCSDEPDWIEW 303
 QY 234 -----RTNKKLLIKPKYTNAFEAAAYKENYALWMPYKYV-SKGIKPTGLWVDFSDIRPYG 286
 DB 304 FDVLLRQTEKKATDLRKGMRFELASKNSQVAPKPGSGRGRKPTK---KDVVDLRTLL 360
 QY 287 NHTGNSAPSYEADNSHGEYGYSDFAVRQHRQ 317
 DB 361 IH---CAQAVAADDRRT---ANELLKQIRQ 384
 RESULT 15
 Q9SKF9 PRELIMINARY; PRT; 863 AA.
 ID Q9SKF9: 01-MAY-2000 (TREMBlrel. 13, Created)
 AC Q9SKF9: 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
 DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
 DE Putative retroelement pol polyprotein.
 GN Name=At2g12920;
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 NX NCBI_TaxID=3702;

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OM protein - protein search, using sw model

Run on: August 18, 2005, 22:33:09 ; Search time 63 Seconds
(without alignments)
379.170 Million cell updates/sec

Title: US-10-617-835-4
Perfect score: 1645
Sequence: 1 MRARLLILPILSVFILSACG.....SHEGYGSDENVRHROGQP 320

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:
1: /cgn2_6/prodata/1/1aa/5A.COMB.pep:*
2: /cgn2_6/prodata/1/1aa/5B.COMB.pep:*
3: /cgn2_6/prodata/1/1aa/6A.COMB.pep:*
4: /cgn2_6/prodata/1/1aa/6B.COMB.pep:*
5: /cgn2_6/prodata/1/1aa/PCTUS.COMB.pep:*
6: /cgn2_6/prodata/1/1aa/Backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1645	100.0	320	4	US-09-043-302-4
2	1645	100.0	320	4	US-09-043-302-7
3	117.5	7.1	1250	3	US-08-938-291A-9
4	117.5	7.1	1250	4	US-09-589-619-9
5	106.5	6.5	190	4	US-09-543-681A-4440
6	106.5	6.5	506	4	US-09-489-039A-12770
7	101	6.1	572	4	US-09-248-796A-15736
8	97	5.9	515	4	US-09-489-039A-10635
9	94.5	5.7	343	4	US-09-071-035-158
10	93.5	5.7	496	4	US-09-252-991A-17814
11	93	5.7	2383	4	US-09-492-709A-302
12	92.5	5.6	927	4	US-09-841-786-3
13	92.5	5.6	3241	4	US-09-841-786-3
14	91.5	5.6	766	4	US-09-489-039A-12983
15	89	5.4	1228	4	US-09-463-402-2
16	89	5.4	1228	4	US-09-689-572-2
17	89	5.4	1228	4	US-09-117-447-2
18	89	5.4	2284	4	US-09-252-991A-23547
19	88.5	5.4	377	4	US-09-540-236-3634
20	88.5	5.4	881	4	US-09-486-072-2
21	87.5	5.3	776	3	US-09-346-237-4
22	87.5	5.3	776	3	US-09-346-237-7
23	86.5	5.3	238	4	US-09-902-540-13083
24	86.5	5.3	977	4	US-09-206-942-53
25	86.5	5.3	983	4	US-09-206-942-51
26	86	5.2	542	4	US-09-538-092-289
27	85.5	5.2	683	4	US-09-252-991A-33038

28	85.5	5.2	781	4	US-09-252-991A-23353	Sequence 23353, A
29	85	5.2	276	4	US-10-243-576-25	Sequence 25, Appl
30	85	5.2	276	4	US-10-243-576-27	Sequence 27, Appl
31	85	5.2	360	4	US-09-902-540-16074	Sequence 16074, A
32	85	5.2	379	1	US-08-685-774-2	Sequence 2, Appl
33	85	5.2	748	4	US-09-252-991A-28449	Sequence 28449, A
34	85	5.2	760	4	US-09-248-796A-19005	Sequence 19005, A
35	85	5.2	2842	1	US-07-741-940-7	Sequence 7, Appl
36	85	5.2	2842	1	US-08-288-548A-7	Sequence 7, Appl
37	85	5.2	2842	1	US-08-452-654-7	Sequence 7, Appl
38	85	5.2	2842	1	US-08-449-731-7	Sequence 7, Appl
39	85	5.2	2843	1	US-08-452-655B-2	Sequence 2, Appl
40	85	5.2	2843	1	US-08-452-655B-7	Sequence 2, Appl
41	85	5.2	2843	3	US-08-450-582-2	Sequence 2, Appl
42	85	5.2	2843	3	US-08-450-582-7	Sequence 2, Appl
43	85	5.2	2843	3	US-09-538-092-1007	Sequence 1007, Ap
44	85	5.2	2973	2	US-08-821-355A-7	Sequence 7, Appl
45	85	5.2	2973	2	US-09-003-687A-7	Sequence 7, Appl

ALIGNMENTS

RESULT 1
US-09-043-302-4
Sequence 4, Application US/09043302
Patent No. 6617128
GENERAL INFORMATION:
APPLICANT: MEYER, Thomas F.
APPLICANT: RUDEL, Thomas
APPLICANT: SCHEUERPLUG, Ina
APPLICANT: MAIER, Jurgen
APPLICANT: EICKENJAGER, Sandra
APPLICANT: SCHMAN, Thomas
TITLE OF INVENTION: Nucleic Acid Molecules Encoding Proteins which Impart
FILE REFERENCE: 0147-172P
CURRENT APPLICATION NUMBER: US/09/043,302
CURRENT FILING DATE: 1998-06-08
EARLIER APPLICATION NUMBER: PCT/EP96/04092
EARLIER FILING DATE: 1995-09-18
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 4
LENGTH: 320
TYPE: PRT
ORGANISM: Neisseria gonorrhoeae
US-09-043-302-4

Query Match
Best Local Similarity 100.0%; Score 1645; DB 4; Length 320;
Matches 320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 MRARLLILPILSVFILSACGTLTGIPSHGGRFAVEBELVAASARAAMKMDLQALHGR 60
1 MRARLLILPILSVFILSACGTLTGIPSHGGRFAVEBELVAASARAAMKMDLQALHGR 60
61 KVALYIATMGOGSSSLTGRYSIDALRGERTINPAVRTDYTRYETTAETSGGLTG 120
61 KVALYIATMGOGSSSLTGRYSIDALRGERTINPAVRTDYTRYETTAETSGGLTG 120
121 LTTSSTNAPALSRTOGSGRSRLGINTGMDYRNETLTTPRDTAFSLHVOYTF 180
121 LTTSSTNAPALSRTOGSGRSRLGINTGMDYRNETLTTPRDTAFSLHVOYTF 180
181 FLRGIDVVS PANADTDVFINTIDFCTINRRTMHLNNAETLKAQTKLEYFAVDRTNKKLL 240
181 FLRGIDVVS PANADTDVFINTIDFCTINRRTMHLNNAETLKAQTKLEYFAVDRTNKKLL 240
241 IKPKTNAEAAKYENALAMGPYKSKIKPEGIMVDFSDIRPYGNHTGNSAPSEADN 300
241 IKPKTNAEAAKYENALAMGPYKSKIKPEGIMVDFSDIRPYGNHTGNSAPSEADN 300

Qy 301 SHEGYSDEAVRHRGQGP 320
Db 301 SHEGYSDEAVRHRGQGP 320

RESULT 2

US-09-043-302-7
Sequence 7, Application US/09043302
Patent No. 6617128
GENERAL INFORMATION:
APPLICANT: MEYER, Thomas F.
APPLICANT: KUDDEL, Thomas
APPLICANT: SCHUEERFLUG, Ina
APPLICANT: MAIER, Jurgen
APPLICANT: EICKERNJAGER, Sandra
APPLICANT: SCHWAN, Thomas
TITLE OF INVENTION: Nucleic Acid Molecules Encoding Proteins Which Impart
TITLE OF INVENTION: the Adhesion of Neisseria Cells to Human Cells
FILE REFERENCE: 0147-172P
CURRENT APPLICATION NUMBER: US/09/043.302
CURRENT FILING DATE: 1998-06-08
EARLIER APPLICATION NUMBER: PCT/EP96/04092
EARLIER FILING DATE: 1995-09-18
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 7
LENGTH: 320
TYPE: PRT
ORGANISM: Neisseria gonorrhoeae
US-09-043-302-7

Query Match 100.0%; Score 1645; DB 4; Length 320;
Best Local Similarity 100.0%; Pred. No. 2.3e-169;
Matches 320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRAALLPILFVSFVILSACGTLTGIPSHGGKRRFAVEDELVAASARA VKMDLQALHGR 60
Db 1 MRAALLPILFVSFVILSACGTLTGIPSHGGKRRFAVEDELVAASARA VKMDLQALHGR 60
Qy 61 KVALYIATMGDQSGSLTGGRYSIDALIRGEYINSPARTYTPRYVETTAETTSGLTG 120
Db 61 KVALYIATMGDQSGSLTGGRYSIDALIRGEYINSPARTYTPRYVETTAETTSGLTG 120
Qy 121 LTTSLSTLNAPALSRTOGDSGSRSSGLNIGMGDYENETLTTPRDTAFLSLVQTVF 180
Db 121 LTTSLSTLNAPALSRTOGDSGSRSSGLNIGMGDYENETLTTPRDTAFLSLVQTVF 180
Qy 121 LTTSLSTLNAPALSRTOGDSGSRSSGLNIGMGDYENETLTTPRDTAFLSLVQTVF 180
Db 121 LTTSLSTLNAPALSRTOGDSGSRSSGLNIGMGDYENETLTTPRDTAFLSLVQTVF 180
Qy 181 FLRGIDVSPANAOTDVFINIDVFETINRRTTMMHLYNAETLKAQTKLEYFAVDRTNKKLL 240
Db 181 FLRGIDVSPANAOTDVFINIDVFETINRRTTMMHLYNAETLKAQTKLEYFAVDRTNKKLL 240
Qy 241 IKPRTNAFEALYKENYALMMGPYKSKGIKPTTEGLMVFSDIRPYNHTGNSAPSEADN 300
Db 241 IKPRTNAFEALYKENYALMMGPYKSKGIKPTTEGLMVFSDIRPYNHTGNSAPSEADN 300
Qy 301 SHEGYSDEAVRHRGQGP 320
Db 301 SHEGYSDEAVRHRGQGP 320

RESULT 3

US-08-938-291A-9
Sequence 9, Application US/08938291A
Patent No. 6117673
GENERAL INFORMATION:
APPLICANT: Lev, Sima
APPLICANT: PLOWMAN, Gregory D.
APPLICANT: SCHOESSINGER, Joseph
TITLE OF INVENTION: RDGB PROTEINS AND RELATED
TITLE OF INVENTION: PRODUCTS AND METHODS
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon

STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0

SOFTWARE: FastSeq

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/938,291A

FILING DATE: September 26, 1997

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/027,337

FILING DATE: October 11, 1996

ATTORNEY/AGENT INFORMATION:

NAME: Wardburg, Richard J.

REGISTRATION NUMBER: 32,327

REFERENCE/DOCKET NUMBER: 228/172

TELECOMMUNICATION INFORMATION:

TELEPHONE: (213) 489-1600

TELEFAX: (213) 955-0440

TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:

LENGTH: 1250 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-938-291A-9

Query Match 7.1%; Score 117.5; DB 3; Length 1250;
Best Local Similarity 23.7%; Pred. No. 0.0055;
Matches 82; Conservative 39; Mismatches 106; Indels 119; Gaps 18;

Qy 14 FILSACGTLTGIPSHGGG-----KRFVBOELVAASARA---AVKD 51
Db 906 FILRQIGKFBGILFVGSNDKDNASFPQGPBREKRIKRSVKKVNAANRADVIVQE 965
Qy 52 -----MDLALHGRKVALYIATMGDQSGSLT-----GGR---YSID- 85
Db 966 GREGRLNARFMYGLDMITLHGEKVDVHI--MKDPPAGQWTFLESTEVTDKNGRISYSIPD 1023
Qy 86 --ALIRGEYINSPAVRDYTY-----PRVETTAETTSGLTGTLTSL--TLNAPAL 133
Db 1024 QVSLGYGIYPKVVVRDHTSVDCYMAVVPPLTECVVFSIDG---SFTASVSVGRDPKV 1080
Qy 134 SRTQSDGSGSRSSIG---LNIIGMGDYENET-----LTTNP--RD 168
Db 1081 RAGAVDVCRHMOELGYLLIITGPRDWOQGRVWSLSQHNFPRLGISFADGLSTDPGLGHK 1140
Qy 169 TAPFLSLVQTVFFLRGIDVVS PANADTVFINIDVFETINRRTTMMHLYNAETLKAQTKLE 228
Db 1141 TAYLNILVQN---HGSIPTAYGSSKD---ISVYTNVGKRTD-----Q 1177
Qy 229 YFAVDRTNKKLLIKPRTNAFEALYKENYALMMGPYKSKGIKPTTEG 274
Db 1178 IFIVGKVKKKL---QSNNA--TVLSDGYAHLAQLQAVGSGSRPAKG 1217

RESULT 4

US-09-589-619-9
Sequence 9, Application US/09589619
Patent No. 6576442
GENERAL INFORMATION:
APPLICANT: Lev, Sima
APPLICANT: PLOWMAN, Gregory D.
APPLICANT: SCHOESSINGER, Joseph

TITLE OF INVENTION: PDGB PROTEINS AND RELATED
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSeq
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/589,619
FILING DATE: 07-Jun-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/938,291
FILING DATE: September 26, 1997
APPLICATION NUMBER: 60/027,337
FILING DATE: October 11, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 228/172
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 1250 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-09-589-619-9

Query Match 7.1%; Score 117.5; DB 4; Length 1250;
Best Local Similarity 23.7%; Pred. No. 0.0055;
Matches 82; Conservative 39; Mismatches 106; Indels 119; Gaps 18;

14 FILSACGLTGTIPSHGGG-----KRAVEQLVAASARA---AVKD 51
906 FILRQIGKEGEPFVGSNDKDNASFRHGOPEKWKTKRTSVKLVANRHRANDVIVOE 965
52 -----MDLQALHGRKVALYATWDOGSGLT-----GGR--YSID- 85
966 GREQLNARFMVGPDMITLHGEKVDVH--MKDPAGQWTLSTEVTDKGRISYSID 1023
86 --ALIRGEYINSPAVRTDYTY-----PRYETTAETSGSLTGLTSL--TINAPAL 133
1024 QVSLGYGYPPVGMVVRGDHSTVDCYMAVVPLTECVFSDG---SFTASMSVTRDRPKV 1080
134 SRTGDSGSGSSSLG---LNTGGMGDYRNET-----LTNRP--RD 168
1081 RAGANDVCRHMOELGLLYITGRPDMOQQRVWSLQHNPFHGLISPADGLSTDPPLGK 1140
169 TAFSLHLYQVTFELGIDVNSPANDTDFINIDVFGTIRNTEMLYNAETLKAQTYKE 228
1141 TAYLNNLVON---HGISTAYGSSKD---ISYTVNWKRTD-----Q 1177
229 YFAVDRTNKLLIKRKTAFAEAYKENVALMMGPYKVSIGKIPTEG 274
1178 IFIVGKVKKL---QSNV---TVLSGYYAAHLAQLQAVGSGSRPAKG 1217

RESULT 5
US-09-543-681A-4440
Sequence 4440, Application US/09543681A
Patent No. 6605709
GENERAL INFORMATION:
APPLICANT: GARY BRETON
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
FILE REFERENCE: 2709.1002-001
CURRENT APPLICATION NUMBER: US/09/543,681A
PRIOR FILING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: US 60/128,706
PRIOR FILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 8344
SEQ ID NO 4440
LENGTH: 190
TYPE: PRT
ORGANISM: Proteus mirabilis
US-09-543-681A-4440

Query Match 6.5%; Score 106.5; DB 4; Length 190;
Best Local Similarity 24.2%; Pred. No. 0.0039;
Matches 50; Conservative 34; Mismatches 84; Indels 39; Gaps 9;

1 MRARLLIPFSVFLSACGLTGTIPSHGGKRAVEQLVAASARA VKMDLQALHGR 60
6 LKKKMLVALFTVSLSGVAASATTVNGGK-INTGEIYNACVSTKSIDQTVNIGQ 64
QY 61 KVALYATWDOGSGLTGRYVSIDALIRGEYINSPAVRTDYPRYETTAETSGSLTG 120
DB 65 YRTAQFDSVGK-----TVGNTDF-----YINLEACDT-----TVQNSVSPSG 103
QY 121 LTTSLSTINAPALSRFOSDGSGRSSSLGLNTGGMGDYRNETLTNPRPTAFLSHLVQTV- 179
DB 104 VSDS-NDKTVLAVSNITTGAGAAATGVGIEI---TDHTGKVL---PPGVSFSTAKQIID 156
QY 180 -----FELR---GIDVVS PANADTDV 197
DB 157 GSNTLNFARYKSTLDVTYPGHADADV 183

RESULT 6
US-09-489-039A-12770
Sequence 12770, Application US/09489039A
Patent No. 6610836
GENERAL INFORMATION:
APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
FILE REFERENCE: 2709.2004001
CURRENT APPLICATION NUMBER: US/09/489,039A
PRIOR FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 12770
LENGTH: 506
TYPE: PRT
ORGANISM: Klebsiella pneumoniae
US-09-489-039A-12770

Query Match 6.5%; Score 106.5; DB 4; Length 506;
Best Local Similarity 22.8%; Pred. No. 0.019; Indels 79; Gaps 14;
Matches 60; Conservative 39; Mismatches 85; Indels 79; Gaps 14;

9 ILFSVFLSACGT-----LTGIPS-HGGG-KRAVEQLVAASARA VKMDLQALH-G 59
DB 257 VLTACVFTSSCVTGPAYRRLNGNSPFGTGKCAFOQ-----KQNDAPHHIG 307
QY 60 KVALYATWDOGSGLTGRYVSIDALIRGEYINSPAVRTDYPRYETTAETT----- 114
DB 308 EKCWVYNAPM-----TIHFVFRDYTTSPRIIRD-GPRSNVYGVITVEKPP 351

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QY 115 -----SGGLTGLTSLSTLNAPALSRTOSSDGS-----RSSLGINIGMGCD 156
; SEQ ID NO 10635
; LENGTH: 515
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
; US-09-489-039A-10635
Db 352 KNIVSLVDGNPLYLIGSLISCSISLSTNSILCSRFQANSQSVNFIKRPASLS-GGFD 410
QY 157 YRNSTLTTPNPDFAFLS-HLVQTVFPLRGIDVSPANADTVFINIDVFGTIRNRTMHL 215
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT FILING DATE: 1999-02-12
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 15736
; LENGTH: 572
; TYPE: PRT
; ORGANISM: Candida albicans
; US-09-248-796A-15736

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RESULT 7
; Sequence 15736, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT FILING DATE: 1999-02-12
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 15736
; LENGTH: 572
; TYPE: PRT
; ORGANISM: Candida albicans
; US-09-248-796A-15736

Query Match 6.1%; Score 101; DB 4; Length 572;
Best Local Similarity 23.8%; Pred. No. 0.094;
Matches 65; Conservative 31; Mismatches 109; Indels 68; Gaps 12;

QY 64 LYIATMGDQSGSLTGRKYSIDALIRGYINSPAVRTTYTPRYETTAETTSGLTGLTT 123
; SEQ ID NO 10635
; LENGTH: 515
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
; US-09-489-039A-10635
Db 53 LSITTNEDINLQSIDPFTVKIDC--SGAFIANDLLRD-TAP--EITDEINN-----S 100
QY 124 SLSTLNAPALSRTOSSDGS-----RSSLGINIGMGCDVNRNLTTPNPDFAFLSHLVQTV 179
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT FILING DATE: 1999-02-12
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 15736
; LENGTH: 572
; TYPE: PRT
; ORGANISM: Candida albicans
; US-09-248-796A-15736
Db 101 SSSITSGTPPLSNTSSDLEDEBESEFTEHNGGLSD---SSSTTVEDDENQLOQLQOP 157
QY 180 FF--LRGIDVSPANADTVFINIDVFGTIRNRTMHLVNAETLKAQTKLEYFAVDRTN 236
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT FILING DATE: 1999-02-12
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 15736
; LENGTH: 572
; TYPE: PRT
; ORGANISM: Candida albicans
; US-09-248-796A-15736
Db 158 LYGAVITKNNTITLPOHNDIHIISVDIGTL-----TKLVYFTKSSSN 200
QY 237 KKLIIKRTNA-----FEAAYKENVALMMGPYKVGKIKPTBGLMADPFDIRP-- 284
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT FILING DATE: 1999-02-12
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 15736
; LENGTH: 572
; TYPE: PRT
; ORGANISM: Candida albicans
; US-09-248-796A-15736
Db 201 RKNSSRRTTGGGGGKGLHFOFOTENFENEMKMKMIKLIKQSIK--SNINPI 252
QY 285 -YGNHTGNSAPSEADNSHEGYGSDEAVRQHR 316
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT FILING DATE: 1999-02-12
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 15736
; LENGTH: 572
; TYPE: PRT
; ORGANISM: Candida albicans
; US-09-248-796A-15736
Db 253 TYIMATGGA-----HKRYNLMKKTKFKKHK 277

```

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RESULT 8
; Sequence 10635, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT FILING DATE: 2000-01-27
; PRIOR FILING DATE: 1999-01-29

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; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 10635
; LENGTH: 515
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
; US-09-489-039A-10635

Query Match 5.9%; Score 97; DB 4; Length 515;
Best Local Similarity 20.5%; Pred. No. 0.21;
Matches 60; Conservative 42; Mismatches 130; Indels 60; Gaps 10;

QY 73 GSGSLTNGRYSIDALIR-----GEYINSPA-----VRTDYTPRYETT--- 110
; SEQ ID NO 10635
; LENGTH: 515
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
; US-09-489-039A-10635
Db 145 GAGGYFTRPSLVMTIVYALIQPSIGELIQDPALGSGFLVSADSPFRNKYSHKYQINPK 204
QY 111 -----ATTSGGLTGLTSLSTLNA-----PALSTRQSGSGSSRLGINIGMG 155
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT FILING DATE: 1999-02-12
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 15736
; LENGTH: 572
; TYPE: PRT
; ORGANISM: Candida albicans
; US-09-248-796A-15736
Db 205 YQGVIEIKNTRRILCMNTFLHRDANIIYGDALTDDAELDKADVIVANPPFGKAGGQR 264
QY 156 DYRNSTLTTPN-RDTAFLSHLVQTVFPLRGIDVSPANADTVFINIDVFGTIRNRTMHL 214
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT FILING DATE: 1999-02-12
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 15736
; LENGTH: 572
; TYPE: PRT
; ORGANISM: Candida albicans
; US-09-248-796A-15736
Db 265 PLKSDIFPPNTNQALQHLIYGLRAGRAAVLPNNVLFESGVGTVDVARLDMMKNLH 324
QY 215 LYNAETLKAQTKLEYFAVDRTNKKLIKPTNAFEAAYKENYA--LMGPKYKSKIKPT 272
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT FILING DATE: 1999-02-12
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 15736
; LENGTH: 572
; TYPE: PRT
; ORGANISM: Candida albicans
; US-09-248-796A-15736
Db 325 ----TILRLPTGLIFAYAGVKTN--VLEFTKGTAKNKYQOENCTEMVWVYDLRTV----- 372
QY 273 EGLMVDPSDIRPQGNHNGNSAPSEADNSHEG-----YGSDEAVRQHRQO 319
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT FILING DATE: 1999-02-12
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 15736
; LENGTH: 572
; TYPE: PRT
; ORGANISM: Candida albicans
; US-09-248-796A-15736
Db 373 ---MPSFGKRTPPGDADIGFAPODGTDPHLGAPEKYGNDPSTKRTGE 421

```

```

RESULT 9
; Sequence 158, Application US/09071035
; Patent No. 6448043
; GENERAL INFORMATION:
; APPLICANT: Gil H. Choi
; TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides
; NUMBER OF SEQUENCES: 496
; CORRESPONDENCE ADDRESS:
; ADDRESS: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/071,035
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: A. Anders Brookes
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PB369P2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 158:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 343 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein

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US-09-071-035-158
Query Match      5.7%; Score 94.5; DB 4; Length 343;
Best Local Similarity 24.5%; Pred. No. 0.21;
Matches 53; Conservative 30; Mismatches 96; Indels 37; Gaps 10;

Qy 10 LFSVFLISAC---GTLTGIPSHGCGK-----RPAVQELVAASARAAMVMDLQALHG 59
Db 14 LFSVTTLAACGGCGGSDSSSASGGKASGEVLRTEQEMPTADLSIATKRISTIALNN 73

Qy 60 RKVALYIATMGD--QSGSGLTGGRYSIDALIRGEYIN-----SPAVRTDYTPRYET 109
Db 74 VYEGYIRLDKONKQYPAGAIAEKAEVSEDLTYKILINDAKMSDCKPYTANDYYGWCQRT 133

Qy 110 TAETTSGLTGITTSLSLTLPALSRITQSDGSRSSLGITGCMGYRNETLTTPROT 169
Db 134 VDPNASEYAVLYASVK--NGDALAKGERD---KSELG--IKAVSD--TELEITLERAT 183

Qy 170 AFLSHLYQ-TVFLRGIDVVS-----PANADTVF 198
Db 184 PFYDYLAPFSFFPQRODIVKYGKAVASNSBSAVY 219

RESULT 10
US-09-252-991A-17814
Sequence 17814, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
PRIOR FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 17814
LENGTH: 496
TYPE: PRF
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-17814

Query Match      5.7%; Score 93.5; DB 4; Length 496;
Best Local Similarity 19.3%; Pred. No. 0.48;
Matches 89; Conservative 40; Mismatches 122; Indels 209; Gaps 21;

Qy 12 SVFLISACGTLTGIPSHGCGKRAVEQELVAASARAAMVMDLQALHGRKXALYIATMGD 71
Db 52 SLFRQAAGELIS---EYGGARR--VEODLTQALK-----QSLSKKKAKNYILLIGD 97

Qy 72 -QSGSGLT-----GGRY-SIDAL-IRGEYINSPAVRTDYTPRYETTAETTSGLT 119
Db 98 GCMGSEITVAANVARGAGGYFKGIDALPLTQGYTHY-SLHKDSGLPDVVTOSASA---T 153

Qy 120 GLTTSLSLTLPN-----ALSRQSDGSGRS----- 145
Db 154 AMTTGVKSYNGAIGVDIHEOPHRNLLBLAKLNGKATGNVSTAELODATPALLAHVTRAK 213

Qy 146 -----SLGNTIGCMGYRNETLTTPNPRDTALSHLVQVFLRGIDVVSPPANA 193
Db 214 CYGEPATSKQCPNALENGAGSITEQWLKTRP-----DVLGGGA 254

Qy 194 DTDVFINIDVGTIRNRTMELYNATETLKAQTKL-----EYFVDRTNKKLILKP 243
Db 255 -----ATPAETAKAGRYAGKTIRAQAEARGYIVENLDELKAVRRANQK---QP 300

Qy 244 KTNAPFAAYKENVALMMP-----YKVSKGIK--- 270
Db 301 LIGLF--AFGNMPPVWIGLPTATYHGNLQNPVASCENPKRTADIPTLLAQMTSKAIELLKD 358

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Qy 271 -----PTGLMVFSD--IRPYG-----NHTGNSAPSEADNSH 302
Db 359 NPNGEFLQVGEASIDKQDHANPCGQIGETVYDLBQKALAFKADGETIYVYADRAH 418

Qy 303 E-----GYGSDAVARQH 315
Db 419 SSQIIPETAPGLTQLLTTKDGAPLAISYGNSESGGEH 458

RESULT 11
US-09-492-709A-302
Sequence 302, Application US/09492709A
Patent No. 6720139
GENERAL INFORMATION:
APPLICANT: Zyskind, Judith
APPLICANT: Ohlsen, Karl L.
APPLICANT: Trawick, John
APPLICANT: Foreyich, R. Allyn
APPLICANT: Froelich, Jamie M.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: GENES IDENTIFIED AS REQUIRED FOR PROLIFERATION IN
FILE REFERENCE: ELITRA.001A
CURRENT APPLICATION NUMBER: US/09/492,709A
CURRENT FILING DATE: 2000-01-27
NUMBER OF SEQ ID NOS: 485
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 302
LENGTH: 2383
TYPE: PRF
ORGANISM: E. Coli
US-09-492-709A-302

Query Match      5.7%; Score 93; DB 4; Length 2383;
Best Local Similarity 23.5%; Pred. No. 7.2;
Matches 72; Conservative 43; Mismatches 102; Indels 90; Gaps 15;

Qy 31 GKPRAVEQELVAASARAAMVMDLQALHGRKVALYIATMGDQSGSGLTGGRYSIDALIRG 90
Db 466 GKSGEVSLSVSLQTKALKGYNEA-----TALEAA-----GKVVYTTGKDIIVTLPAY 515

Qy 91 EYINSPAVRTDYTPRYETTAETTSGLTGITTSLSLTLPALSRITQSDGSGRSSLGIN 150
Db 516 RFTSTP--ETDNTWP-LEVTADYKGNLSNREGSMVVQAFTLS--QKSSVSLSSTQTLN 570

Qy 151 -----IGMGDYRNE-----TLT-----TNPRDTAFISH 174
Db 571 ADSHSTATLTFTIADDAAGNPVGLVLSRHEGVQDITLSWKDNGDSYTOILLTGAMSG 630

Qy 175 LVQTVFPLRGID-----VSPANADTVFINID-----VGTIRNRTMELHY 216
Db 631 TLTLMPQNGVDAKAPAVVVIISVSSRTHSIXIKDRYLSGNPIEVTVELRDE---- 686

Qy 217 NAEITLKQTKLEYAVRNTKGLILKP-----KTNAPFAAYKENVALMMPYKVSIGIK 270
Db 687 NDKPVKQKQQLNNAVSIDN---VKPGVTTWKEFA-DGVYKATYTAI-----TKSGG 735

Qy 271 PTGLMVF 277
Db 736 LTAKLIM 742

RESULT 12
US-09-841-786-3
Sequence 3, Application US/09841786
Patent No. 6669940
GENERAL INFORMATION:
APPLICANT: NAGARAJA, T. G.
APPLICANT: STEWART, GEORGE C.
APPLICANT: NARAYANAN, SANJEEV K.
APPLICANT: CHENGAPPA, M. M.

```

TITLE OF INVENTION: RECOMBINANT FUSOBACTERIUM NECROPHORUM LEUKOTOXIN
TITLE OF INVENTION: VACCINE AND PREPARATION THEREOF
FILE REFERENCE: 30296
CURRENT APPLICATION NUMBER: US/09/841,786
CURRENT FILING DATE: 2001-04-24
PRIOR APPLICATION NUMBER: 09/558,257
PRIOR FILING DATE: 2000-04-25
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 3
LENGTH: 927
TYPE: PRT
ORGANISM: Fusobacterium necrophorum
US-09-841-786-3

Query Match 5.6%; Score 92.5; DB 4; Length 927;
Best Local Similarity 22.5%; Pred. No. 1.7;
Matches 80; Conservative 48; Mismatches 119; Indels 109; Gaps 19;

11 FSVFLLACGTLTGIPSHGGKRAVEOE-----LVAASAR-AAVKMDLQALHGRKVAL 64
558 FHTTSSGANGERDVSSVGVAVSM-VEQENYSKVSVGAKLAKDLNLIKAKETVN 616
65 YIATMG---DQSGSLTGRYSIDALIRGEYINSPAVRTDYTPRYETTAETTSGLTGL 121
617 LVNIGLARSTSGSAVGRLNVO---RSK--NSAIVEA-----KEKAE-----LSG- 658
122 TTSISTNAPALST--QSDGSGRSSSLGILNGMGDY----- 157
659 ---ENINADALNRLFHVAGSPNGSGGNALNGSGYSGGISGARVSIDBEAYLKANKI 714
158 ---RNETLTTPRDTAFL---SHLVQTFPLRGIDVSPA-----NADTD 196
715 ALNSKNDTSVWNAAGSAGICTKMAAVGAVAVNDYDISNKASIEDNDEGSKYDKNDE 774
197 VFINID-----VFGITRRTTEMLYN-----AETLKAQTLKLEYFAVDRNKKLLIK 242
775 VTYAESLEVDATKTGTIINSISVAGINKVSKPSEKPEERPEGFPGKIGNKVDVSK 834
243 PK-TNAEPAAYKE--NYALMMGPYKVGKIKPTGELMVDPSDIRPYGNHTGNSAPS 295
835 NKITSDMSDLTEKITNY-----ISEGVKAKNLPNSVS-----HTPDKGPS 875

RESULT 13
US-09-841-786-1
Sequence 1, Application US/09841786
Patent No. 6669940
GENERAL INFORMATION:
APPLICANT: NAGARAJA, T. G.
APPLICANT: STEWART, GEORGE C.
APPLICANT: NARAYANAN, SANJEEV K.
APPLICANT: CHENGARAPPA, M. M.
TITLE OF INVENTION: RECOMBINANT FUSOBACTERIUM NECROPHORUM LEUKOTOXIN
TITLE OF INVENTION: VACCINE AND PREPARATION THEREOF
FILE REFERENCE: 30296
CURRENT APPLICATION NUMBER: US/09/841,786
CURRENT FILING DATE: 2001-04-24
PRIOR APPLICATION NUMBER: 09/558,257
PRIOR FILING DATE: 2000-04-25
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 1
LENGTH: 3241
TYPE: PRT
ORGANISM: Fusobacterium necrophorum
US-09-841-786-1

Query Match 5.6%; Score 92.5; DB 4; Length 3241;
Best Local Similarity 22.5%; Pred. No. 13;
Matches 80; Conservative 48; Mismatches 119; Indels 109; Gaps 19;
11 FSVFLLACGTLTGIPSHGGKRAVEOE-----LVAASAR-AAVKMDLQALHGRKVAL 64

864 FHTTSSGANGERDVSSVGVAVSM-VEQENYSKVSVGAKLAKDLNLIKAKETVN 922
65 YIATMG---DQSGSLTGRYSIDALIRGEYINSPAVRTDYTPRYETTAETTSGLTGL 121
923 LVNIGLARSTSGSAVGRLNVO---RSK--NSAIVEA-----KEKAE-----LSG- 964
122 TTSISTNAPALST--QSDGSGRSSSLGILNGMGDY----- 157
659 ---ENINADALNRLFHVAGSPNGSGGNALNGSGYSGGISGARVSIDBEAYLKANKI 1020
158 ---RNETLTTPRDTAFL---SHLVQTFPLRGIDVSPA-----NADTD 196
1021 ALNSKNDTSVWNAAGSAGICTKMAAVGAVAVNDYDISNKASIEDNDEGSKYDKNDE 1080
197 VFINID-----VFGITRRTTEMLYN-----AETLKAQTLKLEYFAVDRNKKLLIK 242
1081 VTYAESLEVDATKTGTIINSISVAGINKVSKPSEKPEERPEGFPGKIGNKVDVSK 1140
243 PK-TNAEPAAYKE--NYALMMGPYKVGKIKPTGELMVDPSDIRPYGNHTGNSAPS 295
1141 NKITSDMSDLTEKITNY-----ISEGVKAKNLPNSVS-----HTPDKGPS 1181

RESULT 14
US-09-489-039A-12983
Sequence 12983, Application US/09489039A
Patent No. 6610836
GENERAL INFORMATION:
APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.2004001
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 12983
LENGTH: 766
TYPE: PRT
ORGANISM: Klebsiella pneumoniae
US-09-489-039A-12983

Query Match 5.6%; Score 91.5; DB 4; Length 766;
Best Local Similarity 24.4%; Pred. No. 1.6;
Matches 51; Conservative 33; Mismatches 72; Indels 53; Gaps 12;

125 LSTINAPALSTQSDGSGRSSSLGILN-----IGMGSYRNETLTTPRDTAFLSHLVQTV 179
374 IGYSAFRLNKNKGDAVGR--LDTNRIIDALISGMGVRGDF-----NTGALSHKYNLG 425
180 FFLR-GIDV---VSPANADTVFINIDV-----FG-----TIRNTEMLYNAAE 219
426 YAAOVHTDATKMRKSAANPTTINIDNDVAMPDAAVGCNHDPLVSRSTQGMML-SD 484
220 TLKAQTLKLEYFAVDRNKKLLIKRKTNAF---EAYYENALMMGPYKVGKIKPTGELM 276
485 TLGFNDKVLFTAAARHQKVVVRVNSATGLEDTSSTYSRTGSRM-----FTGELV 534
277 V-DESDIRPYGNHT-----GNSAPSVAD 299
535 YKPWEQLSVYANHTEALQPGSVADPTAAN 563

RESULT 15
US-09-463-402-2
Sequence 2, Application US/09463402
Patent No. 6596510
GENERAL INFORMATION:
APPLICANT: Lubitz, Werner
APPLICANT: Resch, Stephanie
TITLE OF INVENTION: Secretion of Carrier-bound Proteins into the Periplasm

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 18, 2005, 22:52:34 ; Search time 111 Seconds

(without alignments)
1128.897 Million cell updates/sec

Title: US-10-617-835-4

Perfect score: 1645

Sequence: 1 MRARLLIPILSVFILSACG.....SHEGYGSDAVRROGCP 320

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1759131 seqs, 391586102 residues

Total number of hits satisfying chosen parameters: 1759131

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

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2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*

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21: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1645	100.0	320	9	US-09-043-302-4
2	1645	100.0	320	9	US-09-043-302-7
3	1645	100.0	320	18	US-10-617-835-4
4	1645	100.0	320	18	US-10-617-835-7
5	1029	62.6	313	15	US-10-320-800-7
6	103.5	6.3	731	16	US-10-437-963-189840
7	101	6.1	329	15	US-10-425-114-38607
8	101	6.1	348	15	US-10-424-599-199578
9	101	6.1	445	15	US-10-282-122A-52671
10	100	6.1	3147	17	US-10-733-923-10253
11	100	6.1	3167	17	US-10-733-923-10252

12	99.5	6.0	245	15	US-10-424-599-254719	Sequence 254719, A
13	99	6.0	872	15	US-10-282-122A-55467	Sequence 55467, A
14	96.5	5.9	651	15	US-10-425-114-45324	Sequence 45324, A
15	95	5.8	685	15	US-10-335-977-4813	Sequence 4813, Ap
16	94.5	5.7	343	14	US-09-071-035-158	Sequence 158, App
17	94.5	5.7	343	14	US-10-206-576-158	Sequence 158, App
18	94.5	5.7	343	17	US-10-912-362-158	Sequence 158, App
19	94.5	5.7	525	15	US-10-425-114-49395	Sequence 49395, A
20	94.5	5.7	535	15	US-10-424-599-253649	Sequence 253649, A
21	94	5.7	431	15	US-10-282-122A-53853	Sequence 53853, A
22	93.5	5.7	764	17	US-10-732-923-23183	Sequence 23183, A
23	93.5	5.7	1074	15	US-10-282-122A-50616	Sequence 50616, A
24	93.5	5.7	1271	17	US-10-875-518-10	Sequence 10, Appl
25	93.5	5.7	5836	15	US-10-378-083-20	Sequence 20, Appl
26	93	5.7	451	15	US-10-282-122A-51597	Sequence 51597, A
27	93	5.7	764	17	US-10-732-923-23179	Sequence 23179, A
28	93	5.7	1000	14	US-10-156-761-13499	Sequence 13499, A
29	93	5.7	1325	9	US-09-741-669-304	Sequence 304, App
30	93	5.7	2383	9	US-09-912-020-302	Sequence 302, App
31	93	5.7	2383	15	US-10-282-122A-42852	Sequence 42852, A
32	93	5.7	2383	16	US-10-771-241-302	Sequence 302, App
33	92.5	5.6	893	16	US-10-637-544-4	Sequence 4, Appl1
34	92.5	5.6	893	17	US-10-819-275-4	Sequence 4, Appl1
35	92.5	5.6	927	9	US-09-841-786-3	Sequence 3, Appl1
36	92.5	5.6	927	15	US-10-647-057-3	Sequence 3, Appl1
37	92.5	5.6	3241	9	US-09-841-786-1	Sequence 1, Appl1
38	92.5	5.6	3241	15	US-10-647-057-1	Sequence 1, Appl1
39	92	5.6	245	16	US-10-425-115-250945	Sequence 250945, A
40	92	5.6	554	14	US-10-032-585-7607	Sequence 7607, Ap
41	92	5.6	1234	16	US-10-408-765A-155	Sequence 155, App
42	91.5	5.6	452	15	US-10-369-493-15597	Sequence 15597, A
43	91.5	5.6	452	15	US-10-369-493-15974	Sequence 15974, A
44	91.5	5.6	452	15	US-10-369-493-16336	Sequence 16336, A
45	91.5	5.6	523	15	US-10-282-122A-77204	Sequence 77204, A

ALIGNMENTS

RESULT 1

US-09-043-302-4 Application US/09043302

Publication No. US20020086349A1

GENERAL INFORMATION:

APPLICANT: MEYER, Thomas F.

APPLICANT: RUDEL, Thomas

APPLICANT: SCHUEERPFUG, Ina

APPLICANT: MAIER, Jurgen

APPLICANT: EICKERNJAGER, Sandra

APPLICANT: SCHMAN, Thomas

TITLE OF INVENTION: Nucleic Acid Molecules Encoding Proteins which Impart

TITLE OF INVENTION: The Adhesion of Neisseria Cells to Human Cells

FILE REFERENCE: 0147-172P

CURRENT APPLICATION NUMBER: US/09/043,302

CURRENT FILING DATE: 1998-06-08

EARLIER APPLICATION NUMBER: PCT/EP96/04092

EARLIER FILING DATE: 1995-09-18

NUMBER OF SEQ ID NOS: 11

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 4

LENGTH: 320

TYPE: prt

ORGANISM: Neisseria gonorrhoeae

US-09-043-302-4

Query Match

Best Local Similarity 100.0%, Pred. No. 1.8e-150;

Matches 320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MRARLLIPILSVFILSACGTTGTPSYGGGRFVVEDELVAASRAA VKMDLALHGR 60

1 MRARLLIPILSVFILSACGTTGTPSYGGGRFVVEDELVAASRAA VKMDLALHGR 60

Qy 61 KVALYIATMGDGGSLTGRYSIDALIRGEYINSPAVRTDYPRYETTAETTSGLTG 120
Db 61 KVALYIATMGDGGSLTGRYSIDALIRGEYINSPAVRTDYPRYETTAETTSGLTG 120
Qy 121 LTTSLSTINAPALSRITQSDGSSRSLSGLNTGMDYRNETLTTPRDTAFLSHVQTVF 180
Db 121 LTTSLSTINAPALSRITQSDGSSRSLSGLNTGMDYRNETLTTPRDTAFLSHVQTVF 180
Qy 181 FLRGIDVVS PANADTDVFINIDVFGTIRNRTEMLYNAETLKQTKLEYFAVDRTNKKLL 240
Db 181 FLRGIDVVS PANADTDVFINIDVFGTIRNRTEMLYNAETLKQTKLEYFAVDRTNKKLL 240
Qy 241 IKPRTNAFEAAYKENYALMGPYKVS KGIKPTGELMVD FSDIRPYGNHTGNSAPSEADN 300
Db 241 IKPRTNAFEAAYKENYALMGPYKVS KGIKPTGELMVD FSDIRPYGNHTGNSAPSEADN 300
Qy 301 SHEGYGSDA VROHROGQP 320
Db 301 SHEGYGSDA VROHROGQP 320

RESULT 2

US-09-043-302-7
; Sequence 7, Application US/09043302
; Publication No. US20020086349A1
; GENERAL INFORMATION:
; APPLICANT: MEYER, Thomas F.
; APPLICANT: RUDEL, Thomas
; APPLICANT: SCHEUERPFUG, Ina
; APPLICANT: MAIER, Jurgen
; APPLICANT: EICKERNJAGER, Sandra
; APPLICANT: SCHWAN, Thomas
; TITLE OF INVENTION: Nucleic Acid Molecules Encoding Proteins Which Impart
; TITLE OF INVENTION: the Adhesion of Neisseria Cells to Human Cells
; FILE REFERENCE: 0147-172P
; CURRENT APPLICATION NUMBER: US/09/043,302
; CURRENT FILING DATE: 1998-06-08
; EARLIER APPLICATION NUMBER: PCT/EP96/04092
; EARLIER FILING DATE: 1995-09-18
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 320
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-09-043-302-7

Query Match 100.0%; Score 1645; DB 9; Length 320;
Best Local Similarity 100.0%; Pred. No. 1.8e-150;
Matches 320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRARLLPIILPSVFLISACGTLTGIPSHGGGKRFVBOELVAASARA VMDIQLAHR 60
Db 1 MRARLLPIILPSVFLISACGTLTGIPSHGGGKRFVBOELVAASARA VMDIQLAHR 60
Qy 61 KVALYIATMGDGGSLTGRYSIDALIRGEYINSPAVRTDYPRYETTAETTSGLTG 120
Db 61 KVALYIATMGDGGSLTGRYSIDALIRGEYINSPAVRTDYPRYETTAETTSGLTG 120
Qy 121 LTTSLSTINAPALSRITQSDGSSRSLSGLNTGMDYRNETLTTPRDTAFLSHVQTVF 180
Db 121 LTTSLSTINAPALSRITQSDGSSRSLSGLNTGMDYRNETLTTPRDTAFLSHVQTVF 180
Qy 181 FLRGIDVVS PANADTDVFINIDVFGTIRNRTEMLYNAETLKQTKLEYFAVDRTNKKLL 240
Db 181 FLRGIDVVS PANADTDVFINIDVFGTIRNRTEMLYNAETLKQTKLEYFAVDRTNKKLL 240
Qy 241 IKPRTNAFEAAYKENYALMGPYKVS KGIKPTGELMVD FSDIRPYGNHTGNSAPSEADN 300
Db 241 IKPRTNAFEAAYKENYALMGPYKVS KGIKPTGELMVD FSDIRPYGNHTGNSAPSEADN 300
Qy 301 SHEGYGSDA VROHROGQP 320
Db 301 SHEGYGSDA VROHROGQP 320

Db 301 SHEGYGSDA VROHROGQP 320

RESULT 3

US-10-617-835-4
; Sequence 4, Application US/10617835
; Publication No. US20050124037A1
; GENERAL INFORMATION:
; APPLICANT: MEYER, Thomas F.
; APPLICANT: RUDEL, Thomas
; APPLICANT: SCHEUERPFUG, Ina
; APPLICANT: MAIER, Jurgen
; APPLICANT: EICKERNJAGER, Sandra
; APPLICANT: SCHWAN, Thomas
; TITLE OF INVENTION: Nucleic Acid Molecules Encoding Proteins Which Impart
; TITLE OF INVENTION: the Adhesion of Neisseria Cells to Human Cells
; FILE REFERENCE: 0147-172P
; CURRENT APPLICATION NUMBER: US/10/617,835
; CURRENT FILING DATE: 2003-07-14
; PRIOR APPLICATION NUMBER: US/09/043,302
; PRIOR FILING DATE: 1998-06-08
; PRIOR APPLICATION NUMBER: PCT/EP96/04092
; PRIOR FILING DATE: 1995-09-18
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 320
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-617-835-4

Query Match 100.0%; Score 1645; DB 18; Length 320;
Best Local Similarity 100.0%; Pred. No. 1.8e-150;
Matches 320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRARLLPIILPSVFLISACGTLTGIPSHGGGKRFVBOELVAASARA VMDIQLAHR 60
Db 1 MRARLLPIILPSVFLISACGTLTGIPSHGGGKRFVBOELVAASARA VMDIQLAHR 60
Qy 61 KVALYIATMGDGGSLTGRYSIDALIRGEYINSPAVRTDYPRYETTAETTSGLTG 120
Db 61 KVALYIATMGDGGSLTGRYSIDALIRGEYINSPAVRTDYPRYETTAETTSGLTG 120
Qy 121 LTTSLSTINAPALSRITQSDGSSRSLSGLNTGMDYRNETLTTPRDTAFLSHVQTVF 180
Db 121 LTTSLSTINAPALSRITQSDGSSRSLSGLNTGMDYRNETLTTPRDTAFLSHVQTVF 180
Qy 181 FLRGIDVVS PANADTDVFINIDVFGTIRNRTEMLYNAETLKQTKLEYFAVDRTNKKLL 240
Db 181 FLRGIDVVS PANADTDVFINIDVFGTIRNRTEMLYNAETLKQTKLEYFAVDRTNKKLL 240
Qy 241 IKPRTNAFEAAYKENYALMGPYKVS KGIKPTGELMVD FSDIRPYGNHTGNSAPSEADN 300
Db 241 IKPRTNAFEAAYKENYALMGPYKVS KGIKPTGELMVD FSDIRPYGNHTGNSAPSEADN 300
Qy 301 SHEGYGSDA VROHROGQP 320
Db 301 SHEGYGSDA VROHROGQP 320

RESULT 4

US-10-617-835-7
; Sequence 7, Application US/10617835
; Publication No. US20050124037A1
; GENERAL INFORMATION:
; APPLICANT: MEYER, Thomas F.
; APPLICANT: RUDEL, Thomas
; APPLICANT: SCHEUERPFUG, Ina
; APPLICANT: MAIER, Jurgen
; APPLICANT: EICKERNJAGER, Sandra
; APPLICANT: SCHWAN, Thomas
; TITLE OF INVENTION: Nucleic Acid Molecules Encoding Proteins Which Impart
; TITLE OF INVENTION: the Adhesion of Neisseria Cells to Human Cells

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FILE REFERENCE: 0147-172P
CURRENT APPLICATION NUMBER: US/10/617,835
CURRENT FILING DATE: 2003-07-14
PRIOR APPLICATION NUMBER: US/09/043,302
PRIOR FILING DATE: 1998-06-08
PRIOR APPLICATION NUMBER: PCT/EP96/04092
PRIOR FILING DATE: 1995-09-18
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO: 7
LENGTH: 320
TYPE: PRT
ORGANISM: Neisseria gonorrhoeae
US-10-617-835-7

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Query Match      100.0%; Score 1645; DB 18; Length 320;
Beet Local Similarity 100.0%; Pred. No. 1,86-150;
Matches 320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MRARLLILPLSVFLISACGTLTGIPSHGGKRFVVEQELVAASRAAVKMDLQALHGR 60
QY 61 KVALYIATMGDGSGLTGGRYSIDALIRGEYINSPAVRTDVTYPRYETTAETTSGLT 120
DB 61 KVALYIATMGDGSGLTGGRYSIDALIRGEYINSPAVRTDVTYPRYETTAETTSGLT 120
QY 121 LTTSLTNAPALSRTOGSGSSRLGINTGMDYRNETLTTPRDTAFSLHVOYVF 180
DB 121 LTTSLTNAPALSRTOGSGSSRLGINTGMDYRNETLTTPRDTAFSLHVOYVF 180
QY 121 LTTSLTNAPALSRTOGSGSSRLGINTGMDYRNETLTTPRDTAFSLHVOYVF 180
DB 121 LTTSLTNAPALSRTOGSGSSRLGINTGMDYRNETLTTPRDTAFSLHVOYVF 180
QY 181 FLRGIDVSPANADTVFINIDVFETIRNRTMHLVNAETLKAQTKLEYFAVDRNKKLL 240
DB 181 FLRGIDVSPANADTVFINIDVFETIRNRTMHLVNAETLKAQTKLEYFAVDRNKKLL 240
QY 241 IKPKTNAFEAAKYENYALMGPKYKSKIKPTGELMVPFSDIRPYGNHTGNSAPSEADN 300
DB 241 IKPKTNAFEAAKYENYALMGPKYKSKIKPTGELMVPFSDIRPYGNHTGNSAPSEADN 300
QY 301 SHEGYGSDAENVQRHOGQP 320
DB 301 SHEGYGSDAENVQRHOGQP 320

```

```

RESULT 5
US-10-320-800-70
Sequence 70, Application US/10320800
Publication No. US20030215469A1
GENERAL INFORMATION:
APPLICANT: ROBINSON, ANDREW
APPLICANT: GORRINGE, ANDREW
APPLICANT: HUDSON, MICHAEL
APPLICANT: REDDIN, KAREN
TITLE OF INVENTION: MULTICOMPONENT MENINGOCOCCAL VACCINE
FILE REFERENCE: 1581.0790001
CURRENT APPLICATION NUMBER: US/10/320,800
CURRENT FILING DATE: 2002-12-17
PRIOR APPLICATION NUMBER: PCT/GB99/03626
PRIOR FILING DATE: 1999-11-02
NUMBER OF SEQ ID NOS: 75
SOFTWARE: PatentIn version 3.1
SEQ ID NO: 70
LENGTH: 313
TYPE: PRT
ORGANISM: Neisseria meningitidis
US-10-320-800-70

```

```

Query Match      62.6%; Score 1029; DB 15; Length 313;
Beet Local Similarity 62.7%; Pred. No. 8,3e-91;
Matches 197; Conservative 49; Mismatches 62; Indels 6; Gaps 2;
QY 5 LILPLFSVFLISACGTLTGIPSHGGKRFVVEQELVAASRAAVKMDLQALHGRKVAL 64
DB 5 LILPLFSVFLISACGTLTGIPSHGGKRFVVEQELVAASRAAVKMDLQALHGRKVAL 64

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DB 6 LILPL-----VLTACGTLTGIPAHGGKRFVVEQELVAASRAAVKEMDLSALKGRKAAL 60
QY 65 YIATMGDGSGLTGGRYSIDALIRGEYINSPAVRTDVTYPRYETTAETTSGLTGLTSS 124
DB 61 YSVWVGDSGSSNIGGRYSIDALIRGHHNPESATQSYPAVDYTTATTKSDALSSVTS 120
QY 125 LSTLNAPALSRTOGSGSSRLGINTGMDYRNETLTTPRDTAFSLHVOYVFPRG 184
DB 121 TSLNAPALSRTOGSGSSRLGINTGMDYRNETLTTPRDTAFSLHVOYVFPRG 180
QY 185 IDVSPANADTVFINIDVFETIRNRTMHLVNAETLKAQTKLEYFAVDRNKKLLIRPK 244
DB 181 IEVVPPEYADTVFVTVDFGTVSRTELHLVNAETLKAQTKLEYFAVDRNKKLLIRPK 240
QY 245 TNAPFAAKENYALMGPKYKSKIKPTGELMVPFSDIRPYGNHTGNSAPSEADNHEG 304
DB 241 TAAVESQYQEDYALMTGPKYKSKIKPTGELMVPFSDIRPYGNHTGNSAPSEADNHEG 300
QY 305 YGSDAENVQRHOG 318
DB 301 -DVGNEVIRRRKGG 313

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RESULT 6
US-10-437-963-189840
Sequence 189840, Application US/10437963
Publication No. US20040123343A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Barbazuk, Brad
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO: 189840
LENGTH: 731
TYPE: PRT
ORGANISM: Oryza sativa
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT4530_8630C.1.pcp
US-10-437-963-189840

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Query Match      6.3%; Score 103.5; DB 16; Length 731;
Beet Local Similarity 23.2%; Pred. No. 1.3;
Matches 63; Conservative 39; Mismatches 103; Indels 66; Gaps 12;
QY 93 INSPARVDYTPRYETTAETTSGLTGLTSLTNAPALSRTOGSGSSRLGTLN-- 150
DB 134 LDSSESTSSYP-HSLASVTSSNISCANVS-----SQRYVGHSEKRSLSGSS 183
QY 151 ---IGMCDYRN-----ETLTTPRDTAFSLHVOYVFPRGIDVSPANADTVFIN 200
DB 184 QPVPSSDVNANMETLBDPLISNGRIPEVLFESPTDFRGVDEAQFLPGSDKVID 243
QY 201 IDVFETIRN-----TEHNLNAETLKAQ-----TKLEYFAVD----- 233
DB 244 LEAGVVAROBAGRAISLNVSKAEVLKYKURROSEDLDMEGRNSKQSAFCSDEPDWTEM 303
QY 234 -----RTNKQLLIKPKTNAFEAAKYENYALMGPKYKSKIKPTGELMVPFSDIRPYG 286
DB 304 FDLVLRQTEKATDLRKMRFEASGNSPVAPKPSGSRGSRKRTK---KDVVDLRKTL 360
QY 287 NHTGNSAPSEADNHEGYGSDAENVQRHOG 317
DB 361 IH---CAQAVAADRRRT---ANELKKQIRQ 384

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20 GTLTGIPSHGGGR - FAVEQELVAASAPAAVKMDLQALHGRKVALYIATNGDQSGSLT 78

Db 102 PKIVAIGGTGISTMLRGKKYTSNITAIYTVADGGSGGEIREDLGLML--PGGDIRNCI 159

RESULT 11
US-10-732-923-10252
Sequence 10252, Application US/10732923
Publication No. US20050108791A1
GENERAL INFORMATION:
APPLICANT: Edgerton, Michael D
TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPE
FILE REFERENCE: 38-151527961C
CURRENT APPLICATION NUMBER: US/10/732,923
CURRENT FILING DATE: 2003-12-10
PRIOR APPLICATION NUMBER: 10/310,154
PRIOR FILING DATE: 2002-12-04

Query Match	6.0% ;	Score 99.5 ;	DB 15 ;	Length 245 ;
Best Local Similarity	27.4% ;	Pred. No. 0.63 ;		
Matches	51 ;	Conservative 19 ;	Mismatches 69 ;	Indels 47 ;
			Gaps	8
Oy	23	TGATSHGGCKRFAYEOELIVAAASAPAAVKMDLQALHGRKVALYATM-----GDQSSG	75	
Db	77	TGSRSGFVFYFAVSED-----ASSALQGMGDQDLHGRIRIVNRYATERSRPGFGDGGYG	131	
Oy	76	SLTGRYSIDALLNGEYINSPAVRTDYTPPYRTTAETTSGLTGLTSLSTLANAPALSR	135	
Db	132	SGSGGGYNRG-----GNVSGCGGYSGGSGYNN-----CGNVSGGY-NVTSYSGGNA-----E	179	
Oy	136	TQSDSGSRSR--LGLINIGCKGDVNETLTNNPRDTAFLSLVQTVFPLRGIDVVSPPANA	193	
Db	180	TSYTGCGNASHYQNNENSGYFGSAASGEFSSNQNDT-----AGA	218	
Oy	194	DTDVFI	199	

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
RELATING TO HELICOBACTER PYLORI FOR
DIAGNOSTICS AND THERAPEUTICS

NUMBER OF SEQUENCES: 10031

CORRESPONDENCE ADDRESS:

ADDRESSEE: LAHIVE & COCKFIELD

STREET: 28 State Street

CITY: Boston

STATE: Massachusetts

COUNTRY: USA

ZIP: 02109-1875

COMPUTER READABLE FORM:

MEDIUM TYPE: CD-ROM ISO9660

COMPUTER: IBM PC Compatible

OPERATING SYSTEM: Windows NT 4.0

SOFTWARE: UNIX

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/335,977

FILING DATE: 30-Dec-2002

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/993,002

FILING DATE: 17-Dec-1997

ATTORNEY/AGENT INFORMATION:

NAME: Mandagouras, Amy E.

REGISTRATION NUMBER: 36,207

REFERENCE/DOCKET NUMBER: GTN-018

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617)227-7400

TELEFAX: (617)742-4214

INFORMATION FOR SEQ ID NO: 4813:

SEQUENCE CHARACTERISTICS:

LENGTH: 685 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

HYPOTHETICAL: YES

ORIGINAL SOURCE:

ORGANISM: Helicobacter pylori

FEATURE:

NAME/KEY: misc_feature

LOCATION: (B) LOCATION 1...685

SEQUENCE DESCRIPTION: SEQ ID NO: 4813:

US-10-335-977-4813

Query Match 5.8%; Score 95; DB 15; Length 685;

Best Local Similarity 20.8%; Pred. No. 7.8;

Matches 64; Conservative 43; Mismatches 126; Indels 74; Gaps 13;

QY 30 GGRRAVQELVAASARAANKMDLQ---ALHGRVALYIATMGDGGSLTGRYSIDA 86
DB 309 GPSQTTQESDLKKSAR-TIKGKLEGVVSLNGOKLDLSALTYESNTSENT-----DA 361
QY 87 LIRGEYINSPAVRTDYTPRYETTAETTSGLTGLTTSLSLTNAPALSRTOGSGSRSS 146
DB 362 IIGA--INAKGELNAFKNAEGKLVINSKTGMLT-----IKGEDALGKASLKD 406
QY 147 LGLNIGMGMDYRNELTTPNPRDTAFSLHVQ---TVFFLRGIDVVSPPANADTVFINID 202
DB 407 LGLSAGWVOSYEAS-----ODTLFMSKVLQKASDSQFTYNGVSIITRPNEVNDVIGVN 460
QY 203 VFGTIRNRTEHMLVNAETLKAKQTKLEYFAVDRTNKKLTKPTNAFEAAVKE----- 254
DB 461 I--TLEQTTT-----PNKPAIISVSHKNOAIIDSLE--EFVKAHNEELPKLDED 505
QY 255 -NYALMGPYKVKSGIKPTGSLMVDPSDIPRYGNHTGNSAPSEVADNSHEGYGS----- 308
DB 506 TRYDADTKIAGIFNGVDIRAIRSSLNNVFSYVHTDNGVESLTK-----YGLSLDDKG 559
QY 309 ----DEA 311
DB 560 VMSLDEA 566

Search completed: August 18, 2005, 22:56:48
Job time : 116 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - nucleic search, using frame_plus.p2n model

Run on: August 18, 2005, 22:54:53 ; Search time 3940 Seconds
(without alignment)

3935.449 Million cell updates/sec

Title: US-10-617-835-4

Perfect score: 1645
Sequence: 1 MRARLLPILSVFPLSNAG.....SHEGYGSDVAVRHQRCQP 320

Scoring table:

BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:
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-O=/cgn2.1/USPRO.epool.p/US10617835/runcat.18082005.115607.8361/app.query.fasta.1.519
-DB=genembl -OPMT=fastcap -SUFFIX=p2n.rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=biolum62 -TRANS=human0.cdi -LIST=45
-DOCALLIGN=200 -THR.SCORBPCT=100 -THR.MAX=100 -THR.MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTMT=pct -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US10617835 @CGN.1.1.5600 @runcat.18082005.115607.8361 -NCPU=6 -ICPU=3
-NO_MMAP -LARGESCOVERY -NEG.SCORBS=0 -WAIT -DSPELOCK=100 -LONGLOG
-DEV.TIMEOUT=120 -WARN.TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

GenEmbl:*
1: gb_ba:*
2: gb_hg:*
3: gb_in:*
4: gb_ov:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_scs:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1645	100.0	1136	6	A61825 Sequence 5
2	1645	100.0	1136	6	AR393746 Sequence 1
3	1645	100.0	3287	6	A61821 Sequence 1
4	1645	100.0	3287	6	AR393745 Sequence

5	1645	100.0	3294	1	AF142582	AF142582 Neisseria
6	1641	99.8	963	6	A96050	A96050 Sequence 83
7	1641	99.8	963	6	AX04397	AX04397 Sequence
8	1634	99.3	963	6	A96046	A96046 Sequence 79
9	1634	99.3	963	6	AX04395	AX04395 Sequence
10	1624	98.7	963	6	A96048	A96048 Sequence 81
11	1624	98.7	963	6	AX04399	AX04399 Sequence
12	1624	98.7	340806	1	NMA122491	AL162752 Neisseria
13	1621	98.5	10869	1	AE002559	AE002559 Neisseria
14	1621	98.5	172325	6	AX044035	AX044035 Sequence
15	1030	62.6	942	6	A96284	A96284 Sequence 31
16	1029	62.6	640	6	A96044	A96044 Sequence 77
17	1029	62.6	942	6	A96280	A96280 Sequence 31
18	1029	62.6	10057	1	AE002420	AE002420 Neisseria
19	1029	62.6	11700	1	AE002393	AE002393 Neisseria
20	1029	62.6	349980	6	AX044029	AX044029 Sequence
21	1029	62.6	349980	6	AX044030	AX044030 Sequence
22	1026	62.4	195767	1	NMA722491	AL162758 Neisseria
23	1022	62.1	942	6	A96282	A96282 Sequence 31
24	650	39.5	591	6	A96278	A96278 Sequence 31
25	122.5	7.4	2233	1	AY069934	AY069934 Mycobacte
26	119.5	7.3	2723	1	AY667480	AY667480 Lyobacte
27	117.5	7.1	3418	3	BT011130	BT011130 Drosophila
28	117.5	7.1	4188	3	AY051422	AY051422 Drosophila
29	117.5	7.1	4276	6	CO595557	CO595557 Sequence
30	117.5	7.1	4300	6	CO595443	CO595443 Sequence
31	117.5	7.1	4310	3	DMRDGAPT	Y08035 D.melanogast
32	114.5	7.0	12993	6	BD262969	BD262969 DNA sequ
33	111.5	6.8	5529	6	AX024260	AX024260 Sequence
34	111.5	6.8	47713	6	BD262937	BD262937 DNA sequ
35	111.5	6.8	47713	6	AX024213	AX024213 Sequence
36	111.5	6.8	213050	1	AL646079	AL646079 Ralstonia
37	111.5	6.8	110000	1	EX897699	Continuation (7 of
38	109	6.6	4078	1	AB007125	AB007125 Seretia
39	107.5	6.5	299925	1	AP005048	AP005048 Scryptomy
40	107.5	6.5	573	6	AR375262	AR375262 Sequence
41	106.5	6.5	1521	6	AR388870	AR388870 Sequence
42	106.5	6.5	2196	6	AK652816	AK652816 Sequence
43	105.5	6.4	2196	8	AK101402	AK101402 Oryza sat
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ALIGNMENTS

RESULT 1	A61825	1136 bp	DNA	linear	PAT 09-MAR-1998
LOCUS	A61825	Sequence 5 from Patent WO9711181.			
DEFINITION	A61825	GI:3715996			
ACCESSION	A61825	GI:3715996			
VERSION	A61825.1	GI:3715996			
KEYWORDS					
SOURCE	Neisseria gonorrhoeae				
ORGANISM	Neisseria gonorrhoeae				
REFERENCE	1				
AUTHORS	Meyer,T.F., Rudel,T., Scheuerpflug,I., Fischer, Eckhard and Maier,J.				
TITLE	NUCLEIC ACID MOLECULES WHICH CODE PROTEINS WHICH MEDIATE THE ADHESION OF NEISSERIA CELLS TO HUMAN CELLS				
JOURNAL	Patent: WO 9711181-A 5 27-MAR-1997;				
COMMENT	MAX PLANCK GEBELSCRAFT (DE)				
FEATURES	Other Publication DE 19534579 970320.				
source	1. 1136				
	/organism="Neisseria gonorrhoeae"				
	/mol_type="unassigned DNA"				
	/strain="MS11"				
	/db_xref="taxon:485"				

Alignment Scores:

Pred. No.: 3.68e-124 Length: 1136
 Score: 1645.00 Matches: 320
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 6 Gaps: 0

US-10-617-835-4 (1-320) x A61825 (1-1136)

QY 1 MetArgAlaArgLeuLeuIleProIleLeuPheSerValPheIleLeuSerAlaCysGly 20
 DB 135 ATGGGGGACGGCGCTGATACATAATCTTTTTCGGTTTATTTATCCGCTGGCGG 194
 QY 21 ThrLeuThrGlyIleProSerHisGlyGlyIlyAspPheAlaValGlnGlnLeu 40
 DB 195 ACACGACAGGATATCCATCCGATGCGGAGCAAAACCTTCGCGTGCAGACAGACTT 254
 QY 41 ValAlaAlaSerAlaArgAlaAlaValIlyAspMetAspLeuGlnAlaLeuHisGlyArg 60
 DB 255 GTGGCCGCTTCGCGAGCTGCGGTAAAGACATGATTTACAGGCATTTACACGACGA 314
 QY 61 LysValAlaLeuYrIleAlaThrMetGlyAspGlnGlySerGlySerLeuThrGlyGly 80
 DB 315 AAAGTTGATGTATGATTGCAACTATGAGCGACCAAGGTTCAAGGATTTGACAGGAGGT 374
 QY 81 ArgTyrSerIleAspAlaLeuIleArgGlyGlyIlyIleAsnSerProAlaValArgThr 100
 DB 375 CGCTACTCATGATGACCTGATTCGCGGCAATCATAAACAGCCCTGCGCTCCGCACC 434
 QY 101 AspTyrThrTyrProArgTyrGlyIlyThrAlaGlnThrSerGlyIlyLeuThrGly 120
 DB 435 GATTACACCTATCCGCTTACGAAACCAACCGCTGAAACAAATCAGCGGTTTACGCGGT 494
 QY 121 LeuThrThrSerLeuSerThrLeuAsnAlaProIleLeuSerArgThrGlnSerAspGly 140
 DB 495 TTAACCACTTCTTATCTACACTTATATGCCCTGACCTCGCGCACCAATCGACCGGT 554
 QY 141 SerGlySerArgSerSerLeuGlyLeuAsnIleGlyIlyMetGlyAspTyrArgAsnGln 160
 DB 555 AGCGGAAGTAGAGAGCTGGGCTTAATATTTGGCGGAGTGGGGATTTATCGAAATGAA 614
 QY 161 ThrLeuThrThrAsnProArgAspThrAlaPheLeuSerHisGlnThrValPhe 180
 DB 615 ACCTTGACGACCAACCCCGCGACACTGCTTTCTTCCACTTGCTACAGACCGTATTT 674
 QY 181 PheLeuArgGlyIleAspValIleSerProAlaAsnAlaAspThrAspValPheIleAsn 200
 DB 675 TTCTGCGCGGATAGACGTTGTTTCTCTGCCAATGCCGATACAGATGTGTTTATTAC 734
 QY 201 IleAspValPheGlyThrIleAsnAsnArgThrGlnMetHisGlnThrAsnAlaGlnThr 220
 DB 735 ATCGACGATTCGGAAGCATACGCAACGAAACCGAAATGCACCTTATACATCGCGAAACA 794
 QY 221 LeuIlyAlaGlnThrIlyLeuGlnIlyThrPheAlaValAspArgThrAsnIlyLeuLeu 240
 DB 795 CTGAAAGCCCAAACTGGAATATTTCCAGTAGACAGAAACCAATTAATAATTTGCTC 854
 QY 241 IleLysProLysThrAsnAlaPheGlnAlaIleTyrIlyAsnGlyIlyAsnTyrAlaLeuThrPhe 260
 DB 855 ATCAAAACCAAAACCAATGCGTTTGAACTGCTCTTAAAGAAATTTACGCAATTTGGATG 914
 QY 261 GlyProTyrIlyValSerIlyGlyIleLysProThrGlnGlyLeuMetValAspPheSer 280
 DB 915 GGGCGGTATTAAGTAAGCAAAAGAAATCAACCGACGGAAGATTATGTCGATTTCTCC 974
 QY 281 AspIleAsnProTyrGlyIlyAsnHisThrGlyIlyAsnSerAlaProSerValGlnAlaAsn 300
 DB 975 GATATCCGCGCATACGCGCAATCATACGGGTAACTCCGCCCATTCGTGAGAGCTGATAC 1034
 QY 301 SerHisGlnGlyIlyTyrGlyIlyTyrSerAspGlnAlaValArgGlnHisArgGlnGlyIlyPro 320
 DB 1035 AGTCATGAGGGGATATGATACAGCATGAAAGCATGTCGACAAACATAGCAAGGGCACTT 1094

RESULT 2
 AR393746 1136 bp DNA linear PAT 18-DEC-2003
 LOCUS AR393746
 DEFINITION Sequence 6 from patent US 6617128.
 ACCESSION AR393746
 VERSION AR393746.1 GI:40120650
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 1136)
 AUTHORS Meyer,T.F., Rudel,T., Schuenepflug,T., Maier,J., Eickernjager,S.,
 Schwan,T. and Fischer,B.
 TITLE Nucleic acid molecules encoding proteins which impart the adhesion
 of neisseria cells to human cells
 JOURNAL Patent: US 6617128-A 6 09-SEP-2003;
 FEATURES Location/Qualifiers
 source 1..1136
 /organism="unknown"
 /mol_type="genomic DNA"

Alignment Scores:
 Pred. No.: 3.68e-124 Length: 1136
 Score: 1645.00 Matches: 320
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 6 Gaps: 0

US-10-617-835-4 (1-320) x AR393746 (1-1136)

QY 1 MetArgAlaArgLeuLeuIleProIleLeuPheSerValPheIleLeuSerAlaCysGly 20
 DB 135 ATGGGGGACGGCGCTGATACATAATCTTTTTCGGTTTATTTATCCGCTGGCGG 194
 QY 21 ThrLeuThrGlyIleProSerHisGlyGlyIlyAspPheAlaValGlnGlnLeu 40
 DB 195 ACACGACAGGATATCCATCCGATGCGGAGCAAAACGCTTCGCGTGCAGACAGACTT 254
 QY 41 ValAlaAlaSerAlaArgAlaAlaValIlyAspMetAspLeuGlnAlaLeuHisGlyArg 60
 DB 255 GTGGCCGCTTCGCGAGCTGCGGTAAAGACATGATTTACAGGCATTTACACGACGA 314
 QY 101 AspTyrThrTyrProArgTyrGlyIlyThrAlaGlnThrSerGlyIlyLeuThrGly 80
 DB 435 GATTACACCTATCCGCTTACGAAACCAACCGCTGAAACAAATCAGCGGTTTACGCGGT 494
 QY 121 LeuThrThrSerLeuSerThrLeuAsnAlaProIleLeuSerArgThrGlnSerAspGly 140
 DB 375 CGCTACTCATGATGACCTGATTCGCGGCAATACATTAACACCCCTGCGCTCCGCACC 434
 QY 141 SerGlySerArgSerSerLeuGlyLeuAsnIleGlyIlyMetGlyAspTyrArgAsnGln 160
 DB 555 AGCGGAAGTAGAGAGCTGGGCTTAATATTTGGCGGAGTGGGGATTTATCGAAATGAA 614
 QY 161 ThrLeuThrThrAsnProArgAspThrAlaPheLeuSerHisGlnThrValPhe 180
 DB 615 ACCTTGACGACCAACCCCGCGACACTGCTTTTCTTCCACTTGCTACAGACCGTATTT 674
 QY 181 PheLeuArgGlyIleAspValIleSerProAlaAsnAlaAspThrAspValPheIleAsn 200
 DB 675 TTCTGCGCGGATAGAGGTTGTTTCTCTCGCAATGCCATACAGATGTGTTATTATAC 734
 QY 201 IleAspValPheGlyThrIleArgAsnArgThrGlnMetHisGlnThrAsnAlaGlnThr 220

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Db      735 ATCGACGRTTGGACGATACGACAGACGGAATGACCTTATACATCCGAAACA 794
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Db      795 CTGAAGCCCAAACTGGAATATTTCCGAGTAGACAGAACCAATTAATAATTTGCTC 854
Qy      241 IleLysProLysThrAsnAlaPheGluAlaAlaIleLysGluAsnTyrAlaLeuTyrPhe 260
Db      855 ATCAAAACCCAAACCAATGCGTTTGAAGCTGCTTAAAGAAATTTAGCATTTGGAGAG 914
Qy      261 GlyProTyrLysValSerLysGlyIleLysProThrGluGlyLeuMetValAspPheSer 280
Db      915 GGGCGGCTTAAGTAAGCAAGAAATCAACCGACGAGAAATTAATGCTCATTTCTCC 974
Qy      281 AspIleArgProTyrGlyAsnHisThrGlyAsnSerAlaProSerValGluAlaAspAsn 300
Db      975 GATATCCGGCCATACGCGCATATACGGGTACTCCGCCCATCCGTAGAGGCTGATAC 1034
Qy      301 SerHisGluGlyTyrGlyTyrSerAspGluAlaValArgGlnHisArgGlnGlyInPro 320
Db      1035 AGTCATGAGGGGTATGATAGATACGCGATGAGCAGTGCACAACTAGACAAAGGCAACT 1094

RESULT 3
LOCUS   A61821                      3287 bp      DNA      linear      PAT 09-MAR-1998
DEFINITION
Sequence 1 from Patent WO9711181.
ACCESSION
A61821
VERSION
A61821.1 GI:3715995
KEYWORDS
Neisseria gonorrhoeae
Neisseria gonorrhoeae
Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
Neisseriaceae; Neisseria.
ORGANISM
Neisseria gonorrhoeae
REFERENCE
1 Meyer, T.F., Rudel, T., Scheuenerflug, I., Fischer, Eckhard and
Maier, J.
NUCLEIC ACID MOLECULES WHICH CODE PROTEINS WHICH MEDIATE THE
ADHESION OF NEISSERIA CELLS TO HUMAN CELLS
Patent: WO 9711181-A 1 27-MAR-1997;
MAX PLANCK GEBELLSCHAFT (DE)
Other publication DE 19534579 970320.
COMMENT
Location/Qualifiers
FEATURES
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1..3287
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/mol_type="unassigned DNA"
/strain="MS11"
/db_xref="Eaxon:485"
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Alignment Scores:
Pred. No.: 1.38e-123 Length: 3287
Score: 1645.00 Matches: 320
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-617-835-4 (1-320) x A61821 (1-3287)
Qy      1 MetArgAlaArgLeuLeuIleProIleLeuPheSerValPheIleLeuSerAlaCysGly 20
Db      583 ATGCGGGCGCGGCTCTGATACCTATCTTTTTCGTTTATTTATTCGCGCCGCGGG 642
Qy      21 ThrLeuThrGlyIleProSerHisGlyGlyGlyLysArgPheAlaValGluGlnGluLeu 40
Db      643 ACACGACACGATTCATCCATCGCATGCGGAGGCAAAACGTTTCGCGTGGAAACAAACT 702
Qy      41 ValAlaAlaSerAlaArgAlaAlaValLysAspMetAspLeuGlnAlaLeuHisGlyArg 60
Db      703 GTGGCGGCTTCTGCGACAGCTCCGCTTAAAGACATGATTTTACAGGCAATTACACGAGCA 762

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Qy      61 LysValAlaLeuTyrIleAlaThrMetGlyAspGlnGlySerLeuThrGlyGly 80
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Qy      81 ArgTyrSerIleAspAlaLeuIleArgGlyGluTyrIleAsnSerProAlaValArgThr 100
Db      893 CGTACTCATTTGATGACCTGATTTGGCGGCAATCATTAACAGCCCTGCGGTCGCAAC 882
Qy      101 AspTyrThrTyrProArgTyrGluThrThrAlaGluThrThrSerGlyLeuThrGly 120
Db      883 GATTACACCTTATCCCGTTACGAAACCAACCGCTGAAACATCAGCGCGTTTACCGGCT 942
Qy      121 LeuThrThrSerLeuSerThrLeuAsnAlaProAlaLeuSerArgThrGlnSerAspGly 140
Db      943 TTACCACTTCTTTATCTAATCTTAATGCCCCCTGCACTCTGCGACCCAAATCAGACGCT 1002
Qy      141 SerGlySerArgSerSerLeuGlyLeuAsnIleGlyGlyMetGlyAspTyrArgAsnGlu 160
Db      1003 AGCGGAATAGAGAGCAGTCTGGGCTTAATATTGGCGGAGTGGGGATTTATCGAAATGAA 1062
Qy      161 ThrLeuThrThrAsnProArgAspThrAlaPheLeuSerHisLeuValGlnThrValPhe 180
Db      1063 ACCTTGACGACCAACCCCGCGACACTGCTTTCTTCCCACTTGCTACAGACCGTATTT 1122
Qy      181 PheLeuArgGlyIleAspValValSerProAlaAsnAlaAspThrAspValPheIleAsn 200
Db      1123 TTCCGCGCGCATAGAGTGTGTTCTCTGCAATGCGATACAGATGTTTATTTATAC 1182
Qy      201 IleAspValPheGlyThrIleArgAsnArgThrGluMetHisLeuTyrAsnAlaGluThr 220
Db      1183 ATCGACGATTCGGAAGCATACGCAACAGAACCGAAATGCACTTATACATCCGAAACA 1242
Qy      221 LeuYsAlaGlnThrLysLeuGluTyrPheAlaValAspArgThrAsnLysLeuLeu 240
Db      1243 CTGAAGCCCAAACTGGAATATTTCCGATGACAGAACCAATTAATAATTTGCTC 1302
Qy      241 IleLysProLysThrAsnAlaPheGluAlaAlaIleLysGluAsnTyrAlaLeuTyrPhe 260
Db      1303 ATCAAAACCCAAACCAATGCGTTTGAAGCTGCTTAAAGAAATTTAGCATTTGGAGATG 1362
Qy      261 GlyProTyrLysValSerLysGlyIleLysProThrGluGlyLeuMetValAspPheSer 280
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Qy      281 AspIleArgProTyrGlyAsnHisThrGlyAsnSerAlaProSerValGluAlaAspAsn 300
Db      1423 GATATCCGGCCATACGCGCATATACGGGTACTCCGCCCATCCGTAGAGGCTGATAC 1482
Qy      301 SerHisGluGlyTyrGlyTyrSerAspGluAlaValArgGlnHisArgGlnGlyInPro 320
Db      1483 AGTCATGAGGGGTATGATACGCGATGACGATGCGACATAGACAAAGGCAACT 1542

RESULT 4
LOCUS   AR393745                      3287 bp      DNA      linear      PAT 18-DEC-2003
DEFINITION
Sequence 1 from patent US 6617128.
ACCESSION
AR393745
VERSION
AR393745.1 GI:40120648
KEYWORDS
Neisseria gonorrhoeae
Neisseria gonorrhoeae
Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
Neisseriaceae; Neisseria.
ORGANISM
Neisseria gonorrhoeae
REFERENCE
1 (bases 1 to 3287)
Meyer, T.F., Rudel, T., Scheuenerflug, I., Maier, J., Eickemeyer, S.,
Schwan, T. and Fischer, E.
NUCLEIC ACID MOLECULES ENCODING PROTEINS WHICH IMPACT THE ADHESION
OF NEISSERIA CELLS TO HUMAN CELLS
Patent: US 6617128-A 1 09-SEP-2003;
Location/Qualifiers
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ORIGIN

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Alignment Scores:

Pred. No.:	1.38e-123	Length:	3287
Score:	1645.00	Matches:	320
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	6	Gaps:	0

US-10-617-835-4 (1-320) x AR393745 (1-3287)

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QY      21  ThrLeuThrGlyIleProSerHiGlyGlyGlySerGlnPheAlaValGlnGlnLeu 40
Db      643  ACACGACAGGGATATTCATCGCATGCGGAGCGCAACCGCTTCGCGGTGAACAAGAACTT 702
QY      41  ValAlaAlaSerAlaArgAlaAlaValLysAspMetAspLeuGlnAlaLeuHiGlyArg 60
Db      703  GTGGCCGCTTTCGCAAGCTGCCCTTAAAGCATGATTTACAGGCATTCACGAGCA 762
QY      61  LysValAlaLeuTyriIeAlaTherMeGlyAspGlnGlySerGlySerLeuThrGlyGly 80
Db      763  AAAGTTGATTTGATTCATTCAGCACTATGGCGCACCAAGGTTGAGGAGTTGACAGGGGT 822
QY      81  ArgTyriSerIleAspAlaLeuIleArgGlyGlyTyriIeAsnSerProAlaValArgThr 100
Db      823  CGCTACCTCATTTGATGACCTGATTCGCGCGCAATACATTAACAGCCCTCGCTCGCAC 882
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Db      883  GATTACACTTATCCCGCTTACGAACCAACCGCTGAACCAATACAGCGGCTTACCGGCT 942
QY      121  LeuThrThrSerLeuSerThrLeuAsnAlaProAlaLeuSerArgThrGlnSerAspGly 140
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Db      1003  AGCGAAGTAGAGACAGCTCTGGCTTAAATATGGCGGAGTGGGAGATTATCGAAATGAA 1062
QY      161  ThrLeuThrThrAsnProArgAspThrAlaPheLeuSerHiSleuValGlnThraValPhe 180
Db      1063  ACCTTGACGACCAACCGCGGACACAGTCCCTTCTTCCCACTTGATCAGACCGTATTT 1122
QY      181  PheLeuArgGlyIleAspValValSerProAlaAsnAlaAspThrAspValPheIleAsn 200
Db      1123  TTCTCGCGCGCATAGACGTTGTTCTCTCCCAATGCCATACAGATGTGTTATTAAAC 1182
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Db      1183  ATCGACGATTCGGAACGATAGCAACGAAACCGAAATGCACTATACATGCGGAAACA 1242
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Db      1243  CTGAAAGCCCAACCAAACTGGAATATTTCCAGTAGACAGCAACCAATAAAAATTTGCTC 1302
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QY      261  GlyProTyriLysValSerLysGlyIleLysProThrGlnGlyLeuMetValAspPheSer 280
Db      1363  GGGCGGATTAAGTAAGCAAGGAATCAAAACCGAAGGAATTAATGCTGATTTCTCC 1422
QY      281  AspIleArgProTyriGlyAsnHiSerGlyAsnSerAlaProSerValGlnAlaAspAsn 300
Db      1423  GATATCCGGGCAATACGGGAATCATACGGGTAACTCCGCCCACTCCGTAGAGGCTGATAC 1482
QY      301  SerHiSclGlyTyriGlyTyriSerAspGlnAlaValArgGlnHiSargGlnGlyPro 320
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Db 1483 AGTCATGAGGGGTATGATACAGCGATGAAGCACTGCGACACATAGACAGGCAACCT 1542

RESULT 5 AF142582 3294 bp DNA linear BCT 18-MAY-1999

LOCUS AF142582 Neisseria gonorrhoeae maf gene cluster, complete sequence.

DEFINITION AF142582 Neisseriaceae; Neisseria.

ACCESSION AF142582.1 GI:4838552

VERSION 1 (bases 1 to 3294)

KEYWORDS Bacteriophage S., Meyer, T.F., Fischer, E., Maier, J., Manning, P.A.,

SOURCE Neisseria gonorrhoeae

ORGANISM Neisseria gonorrhoeae

REFERENCE Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;

AUTHORS 1 (bases 1 to 3294)

TITLES Bacteriophage S., Meyer, T.F., Fischer, E., Maier, J., Manning, P.A.,

JOURNAL Direct Submission

FEATURES Submitted (13-APR-1999) Molekulare Biologie, MPI fuer

source Infektionsbiologie, Monbijoustr. 2, Berlin 10117, Germany

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ORIGIN

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 QY 221 LeuYsaIaGlnThrLysLeuGluTyrPheAlaValAspArgThrAsnLysLysLeu 240
 DB 661 CTGAAGCCCAAACTGGATATTTCCGAGTAGACAGAACCAATTAATAAATTGCTC 720
 QY 241 IleLysProLysThrAsnAlaPheGluAlaAlaTyrLysGluAsnTyrAlaLeuTyrPhe 260
 DB 721 ATCAAAACCAAAACCAATGCGTTGAGCTGCTTAAAGAAATTTAGCATTTGGATG 780
 QY 261 GlyProTyrLysValSerLysGlyLysProThrGluGlyLeuMetValAspPheSer 280
 DB 781 GGGCGGCTAAAGTAGAGCAAGCAAGCAATCAACCGACGAAAGATTGATGCTGATTC 840
 QY 281 AspIleArgProTyrGlyAsnHisThrGlyAsnSerAlaProSerValGluAlaAspAsn 300
 DB 841 GATATCCAAACCAATCGGCAATCATACGGGTAACTCCGCCCATCCGTAGAGGCTGATAC 900
 QY 301 SerHisGluGlyTyrGlyTyrSerAspGluAlaValArgGlnHisArgGluGlyPro 320
 DB 901 AGTCATGAGGGGTATGATACAGCGATGAGCAAGTGCACAAACATTAACAAGGCACT 960
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 AX043997 963 bp DNA linear PAT 24-NOV-2000
 LOCUS DEFINITION Sequence 76 from Patent WO0066791.
 ACCESSION AX043997
 VERSION AX043997.1 GI:11342888
 KEYWORDS
 SOURCE
 ORGANISM
 Neisseria gonorrhoeae
 Neisseria gonorrhoeae
 Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
 Neisseriaceae; Neisseria.
 REFERENCE
 1 Pizzo, M., Hickey, E., Peterson, J., Tettelin, H., Venter, J. C.,
 Masignani, V., Galeotti, C., Mora, M., Ratti, G., Scarlato, V.,
 Scarlato, V., Rappuoli, R., Frazer, C. M. and Grandi, G.,
 Neisseria genome sequences and methods of their use
 Patent: WO 006791-A 76 09-NOV-2000;
 TITLE
 JOURNAL
 CHIRON CORPORATION (US) ; THE INSTITUTE FOR GENOMIC RESEARCH (US)
 FEATURES
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 Best Local Similarity: 99.69% Mismatches: 0
 Query Match: 99.76% Indels: 0
 Gaps: 0
 DB: 6
 US-10-617-835-4 (1-320) x AX043997 (1-963)
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DB 181 AAAGTGCATTTGATTCATTCGAACCTATGGCGCACCAAGGTTCAAGCATTTACAGGGGT 240
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 QY 221 LeuYsaIaGlnThrLysLeuGluTyrPheAlaValAspArgThrAsnLysLysLeu 240
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 unidentified
 unidentified
 ORIGIN
 Neisseria meningitidis
 Neisseria meningitidis
 1
 REFERENCE
 1 Pizzo, M., Scarlato, V., Rappuoli, R., Grandi, G. and Masignani, V.,
 Neisseria meningitidis
 Patent: WO 924578-A 79 20-SEP-1999;
 TITLE
 JOURNAL
 PIZZA MARIARAZZA (IT); SCARLATO VINCENZO (IT); RAPPUOLI RINO (IT);
 CHIRON SPA (IT); GRANDI GUIDO (IT); MASIGNANI VEGA (IT)
 FEATURES
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 /db_xref="taxon:32644"
 ORIGIN

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 Best Local Similarity: 99.06% Mismatches: 1
 Query Match: 99.33% Indels: 0
 DB: 6 Gaps: 0

US-10-617-835-4 (1-320) x A96046 (1-963)

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LOCUS
DEFINITION Sequence 74 from Patent WO0066791.
ACCESSION AX043995
VERSION AX043995.1 GI:11342887
KEYWORDS
SOURCE
ORGANISM Neisseria meningitidis
Neisseria meningitidis
Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
Neisseriaceae; Neisseria.
REFERENCE
1 Pizza, M., Hickey, E., Peterson, J., Tecteljin, H., Venter, J. C.,
Maignani, V., Galeotti, C., Mora, M., Ratti, G., Scarfelli, M.,
Scarlato, V., Rappuoli, R., Praser, C. M. and Grandi, G.
Neisseria genomic sequences and methods of their use
JOURNAL Patent: WO 0066791-A 74 09-NOV-2000;
CHIRON CORPORATION (US); THE INSTITUTE FOR GENOMIC RESEARCH (US)
FEATURES
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location/Qualifiers
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/organism="Neisseria meningitidis"
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ORIGIN

Alignment Scores:
Pred. No.: 2,346-123 Length: 963
Score: 1634.00 Matches: 317
Percent Similarity: 99.69% Conservative: 2
Best Local Similarity: 99.06% Mismatches: 1
Query Match: 99.33% Indels: 0
DB: 6 Gaps: 0

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QY 61 LysValAlaLeuTyrlleAlaThmerGlyAspGlnGlySerGlySerLeuThrglyGly 80
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ACCESSION	AX043999		
VERSION	AX043999.1		GI:11342889
KEYWORDS			
SOURCE			
ORGANISM			
REFERENCE			
AUTHORS	1		
TITLE	Piazza,M., Hickey,E., Peterson,J., Tettelin,H., Venter,J.C.,		
JOURNAL	Maignani,V., Galeotti,C., Mora,M., Ratti,G., Scariselli,M.,		
FEATURES	Sciariato,V., Rappunoli,R., Frazer,C.M. and Grandi,G.		
source	Patent: WO 0066791-A 78 09-NOV-2000;		
	CHIRON CORPORATION (US) ; THE INSTITUTE FOR GENOMIC RESEARCH (US)		
	Location/Qualifiers		
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Query Match: 98.72% Indels: 0
DB: 6 Gaps: 0

US-10-617-835-4 (1-320) x AX043999 (1-963)

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OY      61 LysValAlaLeuTyrlleAlaThrMetGlyAspGlnGlySerGlySerLeuThrGlyGly 80
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DB      481 ACCTTGACGACCTAACCCGCGGACACCTGCTTTCTTCCCACTTGCTACAGACCTGATTT 540
OY      181 PheLeuArgGlyIleAspValValSerProAlaAlaAlaAspThrAspValPheIleAla 200
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DEFINITION Neisseria meningitidis serogroup A strain 22491 complete genome;
segment 1/7.
ACCESSION AL162752 AL157959
VERSION AL162752.2 GI:7378778
KEYWORDS

SOURCE
ORGANISM
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Neisseria meningitidis Z2491
Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
Neisseriaceae; Neisseria.
REFERENCE
AUTHORS
1 (bases 1 to 340806)
Parkhill,J., Achtman,M., James,K.D., Bentley,S.D., Churcher,C., Klee,S.R., Korell,J.G., Baoham,D., Brown,D., Chillingworth,T., Davies,R.M., Davis,P., Devlin,K., Feltham,T., Hamlin,N., Holtroyd,S., Jagers,K., Leach,S., Moule,S., Mungall,K., Quail,M.A., Rajandream,M.A., Rutherford,K.M., Simmonds,M., Skellon,J., Whitehead,S., Spratt,B.G. and Barrall,B.G.
Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491
Nature 404 (6777), 502-506 (2000)

TITLE
JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS
TITLE
JOURNAL
2 (bases 1 to 340806)
Parkhill,J.
Direct Submission
Submitted (30-MAR-2000) Submitted on behalf of the Neisseria sequencing team, Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA E-mail: parkhill@sanger.ac.uk

COMMENT
Notes:
Details of N. meningitidis sequencing at the Sanger Centre are available on the World Wide Web.
(URL, http://www.sanger.ac.uk/Projects/N_meningitidis/).
Location/Qualifiers

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(EMBL:AF036487) Lactococcus lactis plasmid pNZ4000
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Score: 1624.00 Matches: 315
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Query Match: 98.72% Indels: 0
DB: 1 Gaps: 0

US-10-617-835-4 (1-320) x NMA122491 (1-340806)
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Db	306921	ATGCAAGACCGCGCTGATTACTATTCTTTTTCAGTTTATTTATTCGCCGTCGGGG	3068722
Qy	21	ThrlLeuthrGlyIleProSerHsGlyGlyGlyValysPheAlaValGluGlnIleu	40
Db	306871	ACACGACGAGGATATTCATCCGATGGCGGAGGTAAACGCTTGGCGGTGCAACAAGAACTT	3068122
Qy	41	ValAlaAlaSerAlaArgAlaAlaValIysAspMetAspLeuGlnIleuHsIsgIYAsG	60
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Qy	61	LysValAlaLeuTyrlleAlaThrMetGlyAspGlnGlySerGlySerLeuthrGlyIy	80
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Qy	81	ArgTyrserrIleasplaleuIleArgGlyGlyTyrlleAsnSerProAlaValaGlyThr	100
Db	306691	CGCTACTCATGAGTGCATGATGCTGGCGAAATCATAAACAGCCCTGCGTCCGTACC	3066322
Qy	101	AspTyrrThTyProArgTyrcGluThrThrAlaGluThrThrserylGlyLeuthrGlyI	120
Db	306631	GATTACACCTATCCAGCTTACGAACCAACCGCTGAACAACAATCAGCGGTTGACAGGT	3065722
Qy	121	LeuthrThrserrLeuSerThrlleuAlaProAlaLeuSerArgThrglnSerAspGlyI	140
Db	306571	TTAACACACTTCTTTATCTACACTTAATGCCCTGTGCACTCGCGCAACCAATCAGACGGT	3065122
Qy	141	SerGlySerArgSerSerIleuGlyLeuAlaenIsgIYMetGlyAspTyrrArgAsnGlyI	160
Db	306511	AGCGGAAGTAAAGACATCTGGGCTTAATATTGGCGGAGTGGGGCATTTTCGAATGGA	3064522
Qy	161	ThrlLeuthrThAsnProArgAspThrAlaPheLeuSerHsIleuValGlnThrValPhe	180
Db	306451	ACCTTGACGACTAACCCCGCGGACACTGCTCTTCTTCCCACTGGTACAGACCGTATTT	3063922
Qy	181	PheLeuArgGlyIleAspValValSerProAlaAlaAlaAspThrAspValPheIleAla	200
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Qy	201	IleAspValPheGlyThrlleArgAsnArgTrgIleMetHsIleuTyrrAsnIlaGluThr	220
Db	306331	ATCGACGATTTGGAACGATACGACACAGAACCGAATATGACCTATTCAATGCCGAAC	3062722
Qy	221	LeuIysAlaGlnThrIleLeuGlnIuTyrrPheAlaValAspArgThrxnIlyIleuLeu	240
Db	306271	CTGAAGCCCAACAAACTGGAATATTTCCGACGTGACAGAACCAATAAATAATGGCTC	3062122
Qy	241	IleIysProIySerThsAsnAlaPheGlyAlaAlaIlyTyrlIyGlnAsnTyrrAlaLeuTrpMet	260
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RESULT 13	LOCUS	DEFINITION	ORGANISM
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AE002559		Neisseria meningitidis serogroup B strain MC58 section 201 of 206	
AE002559		of the complete genome.	
AE002559		AE002098	
AE002559.2		GI:7413482	
Neisseria meningitidis	MC58		
Neisseria meningitidis	MC58		

REFERENCE	Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales; Neisseriaceae; Neisseria.
AUTHORS	1 (bases 1 to 10869)
TITLE	Tettelin,H., Saunders,N.J., Heidelberg,J., Jeffries,A.C., Nelsson,K.E., Eisen,J.A., Ketchum,K.A., Hood,D.W., Peden,J.F., Dodson,R.J., Nelsson,W.C., Gwinn,M.L., Deboy,R., Peterson,J.D., Hickey,E.K., Haft,D.H., Salzberg,S.L., White,O., Fleischmann,R.D., Dougherty,B.A., Mason,T., Clicko,A., Parksey,D.S., Blair,E., Cltcone,H., Clark,E.B., Cotton,M.D., Uterback,T.R., Khouri,H., Qin,H., Vamshayan,J., Gill,J., Scarlato,V., Maignani,V., Piazza,M., Grandt,G., Sun,L., Smith,H.O., Frazer,C.M., Moxon,E.R., Rappulli,R. and Venter,J.C.
JOURNAL	Complete genome sequence of Neisseria meningitidis serogroup B strain MC58
MEDLINE	Science 287 (5459), 1809-1815 (2000)
PUBMED	2015755
REFERENCE	10710307
AUTHORS	2 (bases 1 to 10869)
TITLE	Tettelin,H., Saunders,N.J., Heidelberg,J., Jeffries,A.C., Nelsson,K.E., Eisen,J.A., Ketchum,K.A., Hood,D.W., Peden,J.F., Dodson,R.J., Nelsson,W.C., Gwinn,M.L., Deboy,R., Peterson,J.D., Hickey,E.K., Haft,D.H., Salzberg,S.L., White,O., Fleischmann,R.D., Dougherty,B.A., Mason,T., Clicko,A., Parksey,D.S., Blair,E., Cltcone,H., Clark,E.B., Cotton,M.D., Uterback,T.R., Khouri,H., Qin,H., Vamshayan,J., Gill,J., Scarlato,V., Maignani,V., Piazza,M., Grandt,G., Sun,L., Smith,H.O., Frazer,C.M., Moxon,E.R., Rappulli,R. and Venter,J.C.
JOURNAL	Direct Submission
COMMENT	Submitted (17-MAR-2000) The Institute for Genomic Research, 9712 Medical Center Dr, Rockville, MD 20850, USA
FEATURES	On Apr 4, 2000 this sequence version replaced gi:7227357.
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gene	/mol_type="genomic DNA"
CDS	/strain="MC58"
gene	/db_xref="taxon:122586"
CDS	/note="serogroup: B"
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Pred. No.: 5.4e-121 Length: 10869
Score: 1621.00 Matches: 317
Percent Similarity: 99.38% Conservative: 2
Best local Similarity: 98.75% Mismatches: 1
Query Match: 98.54% Indels: 1
DB: 1 Gaps: 0

US-10-617-835-4 (1-320) x AE002559 (1-10869)

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Qy 21 ThrLeuThrGlyIleProSerHisGlyGlyLyAsArgPheAlaValGluGlnGluLeu 40
Db 7322 ACACTGACAGTATTCATCGCATGGCGGAGGTAAACGTTTGCGGTCGAACAAGAACTT 7381
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QY      100  RASPTYrThrYrProArgYrGluThrThraIaGluThrThrSerGlyGlyLeuThG1 120
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QY      120  YleuThrThrSerLeuSerThrLeuAsnAlaProAlaLeuSerArgThrGlnSerAspG1 140
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QY      140  YserGlySerArgSerSerSerLeuGlyLeuAsnTleGlyGlyMetGlyAspTyrArgAsnG1 160
Db      7682  TAGCGGAAGTAAACACAGCTGGGCTTAATAATTTGGCGGATGGGCGATTAACGAAATGA 7741
QY      160  UThrLeuThrThraAnProArgAspThraIaPheLeuSerHisLeuValGlnThValPh 180
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QY      240  nIleAspProYrThraAsnAlaPheGluAlaIaTyrYrGlyGlnAsnTyrAlaLeuTyrMe 260
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QY      260  CGlyProTyrYrValSerTyrGlyTlleYrProThrGluGlyLeuMetValAspPheSe 280
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QY      280  RASPTYrThrYrProArgYrGlyAsnHisThrGlyAsnSerAlaProSerValGluAlaAspAs 300
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ACCESSION  AX044035
VERSION     AX044035.1  GI:11342919
KEYWORDS
SOURCE
ORGANISM   Neisseria meningitidis
            Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
            Neisseriaceae; Neisseria.

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REFERENCE
AUTHORS    Pizzo, M., Hickey, E., Peterson, J., Tetteijn, H., Venter, J.C.,
            Maignani, V., Galeotti, C., Mora, M., Ratti, G., Scarselli, M.,
            Scariolo, V., Rappuoli, R., Frazer, C.M. and Grandi, G.
TITLE      Neisseria genomic sequences and methods of their use
JOURNAL    Patent: WO 0066791-A 114 09-NOV-2000;
            CHIRON CORPORATION (US) ; THE INSTITUTE FOR GENOMIC RESEARCH (US)
FEATURES
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ORIGIN

Alignment Scores:

Pred. No.:	1,686-119	Length:	172325
Score:	1621.00	Matches:	317
Percent Similarity:	99.38%	Conservative:	2
Best Local Similarity:	98.75%	Mismatch:	1
Query Match:	98.54%	Indel:	1
DB:	6	Gaps:	0

US-10-617-835-4 (1-320) x AX044035 (1-172325)

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QY      100  RASPTYrThrYrProArgYrGluThrThraIaGluThrThrSerGlyGlyLeuThG1 120
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RESULT 15
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DEFINITION Sequence 317 from Patent WO924578.
ACCESSION A96284
VERSION A96284.1 GI:6780034
KEYWORDS
SOURCE unidentified
ORGANISM unidentified.
REFERENCE
1 Pizza,M., Scariato,V., Rappuoli,R., Grandi,G. and Maignani,V.
AUTHORS Neisserial antigens
TITLE Patent: WO 92/4578-A 317 20-MAY-1999;
JOURNAL PIZZA MARIAGRAZIA (IT); SCARILATO VINCENZO (IT); RAPPUOLI RINO (IT);
CHIRON SPA (IT); GRANDI GUIDO (IT); MALIGNANI VEGA (IT)
FEATURES
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ORIGIN
Alignment Scores: 2.19e-74 Length: 942
Pred. No.: 1030.00 Matches: 197
Score: 78.66% Conservative: 50
Percent Similarity: 62.74% Mismatches: 61
Best Local Similarity: Indels: 6
Query Match: 62.61% Gaps: 2
DB: 6

US-10-617-835-4 (1-320) x A96284 (1-942)
Oy      5  LeuLeuIleProIleLeuPheSerValPheIleLeuSerAlaCyGlyThrIleuThrGly 24
Db      16  CTCCTCATCCCCCTC-----GTACTCACCGCTCGGCGACACTGACCGCGC 60
Oy      25  IleProSerHisGlyGlyIleValArgPheAlaValGluGlnGluLeuValAlaAsp 44
Db      61  ATACCGCGCCACGGCGGCGGCAAGCTTTGGCGGTGCAACAGAACTGTCGCGCGCATCG 120
Oy      45  AlaArgAlaAlaValIleValAspMetAspLeuGlnAlaLeuHisGlyValArgValAlaLeu 64
Db      121  TCCCGCGCGCGTAAAGAAATGGAATTGTCCGCCCTGAAGAGACGCAAAAGCCGCCCTT 180
Oy      65  TyrIleAlaThrMetGlyAspGlnGlySerGlySerLeuThrGlyIleArgTyrSerIle 84
Db      181  TACGCTCTCGTTATGGCGACCAAGTTCCGGCAACATAGCGGCGGACGCTACTCCATC 240
Oy      85  AspAlaLeuIleArgGlyGlyTyrIleAsnSerProAlaValArgThrAspTyrThrTyr 104
Db      241  GACCGACTGATACGGCGGCGGTACCAACAACCCGACAGCGGCCGATACAGCTAC 300
Oy      105  ProArgTyrGluThrThrAlaGluThrThrSerGlyIleuThrGlyLeuThrThrSer 124
Db      301  CCCGCTATGACACTACCGCACCAACAATCCAGCGGCTCTCCGGCGTAAACCACTTCC 360

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Oy      125  LeuSerThrIleuAsnAlaProAlaLeuSerArgThrGlnSerAspGlySerArg 144
Db      361  ACATCGCTTTTGAACGCCCCCGCGCGCCCTGTACGAAACAAACGACGCAAAAGCGAA 420
Oy      145  SerSerLeuGlyLeuAsnIleGlyIleMetGlyAspTyrArgAsnGluThrIleuThr 164
Db      421  CGCTCCCGCGGACGTCCGTCMAAGCGGACGGGCGCATACCGCAACGAAACCTTCCTCGCC 480
Oy      165  AspProArgAspThrAlaPheLeuSerHisIleuValGlnThrValPhePheLeuArgGly 184
Db      481  AACCCTCGGACGTTCTCTTCTTACCAACTCATCCAAACGCTCTTCTTACCTCGCGGC 540
Oy      185  IleAspValIleSerProAlaAsnAlaAspThrAspValPheIleAsnIleAspValPhe 204
Db      541  ATCGAAGTCGTAACCGCCCGAATACCGGACACCGACGTAATTCGTAACCGTGAATTC 600
Oy      205  GlyThrIleArgAsnArgThrGluMetCHisLeuTyrAsnAlaGluThrLeuValGln 224
Db      601  GGCACCGTCCGCAACCGCTACCGAATGCACTCCTTACCAACCGCGAAACCTTAAAGCCCAA 660
Oy      225  ThrIleuGluGluTyrPheAlaValAspArgThrAsnIleValIleuIleValProIys 244
Db      661  ACCAAGCTCGAATATTTGCGCGTGCAGCGGACGACAGCGAAACTGTGATTTGCCCTTAA 720
Oy      245  ThrAsnAlaPheGluAlaAlaTyrIleGluAsnTyrAlaLeuThrMetGlyProTyrIys 264
Db      721  ACCGCGCGCTTACGAAATCCCAATACCAAGAACATACCCCTCTGATGGGACCTTACAGC 780
Oy      265  ValSerIleGlyIleValProThrGlnGlyIleuMetValAspPheSerAspIleArgPro 284
Db      781  GTCGCAAAACCGCAAGGCTCAGACCGGCTGATGGTGTGATTTCTTCGACATCACCC 840
Oy      285  TyrGlyAsnHisThrGlyAsnSerAlaProSerValGluAlaAspAsnSerHisGly 304
Db      841  TACGGCACACACACCGCCCAAAACCGTCCGACTTCAAAACAAACACCGT---AAAAC 897
Oy      305  TyrGlyTyrSerAspGluAlaValArgGlnHisArgGlnGly 318
Db      898  CCCGATGTCGCAACGAAATGTCATCCGCGCGCAAGAGGA 939

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Search completed: August 19, 2005, 00:57:11
Job time : 4081 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame_plus.p2n model

Run on: August 18, 2005, 22:56:54 ; Search time 534 Seconds
(without alignment)
3547.411 Million cell updates/sec

Title: US-10-617-835-4

Perfect score: 1645
Sequence: 1 MRALLPILPSVFLISACG.....SHEGYSDPAVRQRGGOP 320

Scoring table:
BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-DB=N.Geneseg.16Dec04 -QFMT=fastaop -SUPFIX=sp2n.rng -MINMATCH=0.1 -LOOPCL=0
-IOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=biosum62 -TRANS=human40.cdi
-LIST=45 -DOCALLIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pct -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
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-NO_WMAP -LARGEQUERY -NEG_SCORES=30 -THREADS=1 -DSPBLOCK=100 -LONOLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :
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10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	1645	100.0	3287	2 AAT70386	Aat70386 Neisseria
2	1641	99.8	960	10 AB237917	Ab237917 N. gonorr
3	1641	99.8	963	2 AA212008	AA212008 Neisseria
4	1641	99.8	963	3 AA254614	AA254614 Neisseria
5	1641	99.8	963	3 AA253688	AA253688 Neisseria

6	1641	99.8	963	3 AA21297	AA21297 N. gonorr
7	1641	99.8	963	3 AAF21582	AAF21582 N. gonorr
8	1634	99.3	963	2 AA212006	AA212006 Neisseria
9	1634	99.3	963	3 AA253689	AA253689 Neisseria
10	1634	99.3	963	3 AA254613	AA254613 Neisseria
11	1634	99.3	963	3 AA21296	AA21296 N. mening
12	1634	99.3	963	3 AAF21581	AAF21581 N. mening
13	1624	98.7	963	2 AA212007	AA212007 Neisseria
14	1624	98.7	963	3 AA254615	AA254615 Neisseria
15	1624	98.7	963	3 AA253690	AA253690 Neisseria
16	1624	98.7	963	3 AA21298	AA21298 N. mening
17	1624	98.7	963	3 AAF21583	AAF21583 N. mening
18	1621	98.5	92934	3 AA21473	AA21473 N. mening
19	1621	98.5	110000	3 AA21489_7	AA21489_7
20	1621	98.5	172325	3 AAF21613	AAF21613 Neisseria
21	1318	80.1	789	10 AB240799	AB240799 N. gonorr
22	1030	62.6	939	10 AB239696	AB239696 N. gonorr
23	1030	62.6	939	10 AB241775	AB241775 N. gonorr
24	1030	62.6	942	2 AA212111	AA212111 Neisseria
25	1029	62.6	640	2 AA212005	AA212005 Neisseria
26	1029	62.6	640	3 AA21330	AA21330 N. mening
27	1029	62.6	942	2 AA212109	AA212109 Neisseria
28	1029	62.6	110000	3 AA21490_03	AA21490_03
29	1029	62.6	110000	3 AA21490_06	AA21490_06
30	1029	62.6	110000	3 AA21489_0	AA21489_0
31	1029	62.6	349980	3 AAF21607	AAF21607 Neisseria
32	1029	62.6	349980	3 AAF21608	AAF21608 Neisseria
33	1022	62.1	942	2 AA212110	AA212110 Neisseria
34	882.5	53.6	882	10 AB239704	AB239704 N. mening
35	789.5	48.0	25509	3 AA21467	AA21467 N. mening
36	650	39.5	591	2 AA212108	AA212108 Neisseria
37	650	39.5	591	3 AA21359	AA21359 N. mening
38	273	16.6	399	3 AA212165	AA212165 N. mening
39	117.5	7.1	4276	4 ABL17383	ABL17383 Drosophila
40	117.5	7.1	4200	4 ABL17307	ABL17307 Drosophila
41	106.5	6.5	573	10 ADE99982	ADE99982 Bacteriophage
42	106.5	6.5	1521	11 ACH99984	ACH99984 Klebsiella
43	105.5	6.4	2196	8 ADA69363	ADA69363 Rice gene
44	104.5	6.4	110000	6 AB269245_01	AB269245_01
45	104.5	6.4	110000	6 AB267197_00	AB267197_00

ALIGNMENTS

RESULT 1	
AA270386	AA270386 standard; DNA; 3287 BP.
XX	
AC	AA270386;
XX	
DT	08-DEC-1997 (first entry)
XX	
DE	Neisseria adhesion proteins.
XX	
KW	Neisseria gonorrhoeae; adhesion; lipoprotein; OrfA; Orf1; OrfB; BB.
XX	
OS	Neisseria gonorrhoeae.
XX	
FH	
FT	Key
FT	-35_signal
FT	/tag= a
FT	78..83
FT	-10_signal
FT	/tag= b
FT	124..128
FT	RBS
FT	/tag= c
FT	136..449
FT	CDS
FT	/tag= d
FT	/label= OrfA
FT	514..519
FT	-35_signal
FT	/tag= e
FT	534..539
FT	-10_signal
FT	/tag= f
FT	571..577
FT	RBS

AA21297 N. gonorr	
AA21582 N. gonorr	
AA212006 Neisseria	
AA253689 Neisseria	
AA254613 Neisseria	
AA21296 N. mening	
AAF21581 N. mening	
AA212007 Neisseria	
AA254615 Neisseria	
AA253690 Neisseria	
AA21298 N. mening	
AAF21583 N. mening	
AA21473 N. mening	
Continuation (8 of	
AA21613 Neisseria	
AB240799 N. gonorr	
AB239696 N. gonorr	
AB241775 N. gonorr	
AA212111 Neisseria	
AA212005 Neisseria	
AA21330 N. mening	
AA212109 Neisseria	
Continuation (4 of	
Continuation (7 of	
AA21489 N. mening	
AAF21607 Neisseria	
AAF21608 Neisseria	
AA212110 Neisseria	
AB239704 N. mening	
AA21467 N. mening	
AA212108 Neisseria	
AA21359 N. mening	
AA212165 N. mening	
ABL17383 Drosophila	
ABL17307 Drosophila	
ADE99982 Bacteriophage	
ACH99984 Klebsiella	
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Continuation (2 of	
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FT FT	/label= OrfB	
XX PN	DE19534579-A1.	
XX PD	20-MAR-1997.	
XX PF	18-SEP-1995; 95DE-01034579.	
XX PR	18-SEP-1995; 95DE-01034579.	
XX PA	(PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.	
XX DR	WPI; 1997-180942/17.	
DR P-PDB:	AAM18784 , AAM18785 , AAM18786 .	
PT CC	Nucleic acids encoding Neisseria adhesion proteins - for therapeutic and diagnostic use.	
PS CS	Claim 1 ; Page 11-13; 2Opp; German.	
CC CC	OrfA and OrfB in complexes with the protein PilC are capable of adhering to human cells. Products obtained from the DNA are useful in medicaments,	
CC CC	diagnostic compns. and vaccines, esp. for treatment of Neisseria gonorrhoea and N. meningitidis infections	
SQ XX	Sequence 3287 BP; 1016 A; 741 C; 752 G; 778 T; 0 U; 0 Other;	
 Alignment Scores:		
Pred. No. :	5,6Se-158	Length: 3287
Score:	1645.00	Matches: 320
Percent Similarity:	100.00%	Conservative: 0
Best Local Similarity:	100.00%	Mismatches: 0
Query Match:	100.00%	Indels: 0
DB:	Gaps: 2	0
US-10-617-835-4 (1-320) x AAT70386 (1-3287)		
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Dd	583 ATGGCGGCAGCGCTGTACTTATTCTTTTGTTTTTAATTTCGCCCTGCCGG	642
OY	21 ThrLeuThrgLyileProSerHisgllylgylglylsyARGpehaLaVaIgUgInJubeu 40	
Dd	643 ACACGTGAAGAgtattccatgcccatggcgaagcaaacgccttgcggcgcmacmaacttt	702
OY	41 ValAlaaLSerilaargalaaLavallysaspMetaspleuglnalleuhisgllyArg 60	
Dd	703 GTGGCGGCTTCGCAGAGCTGCCGTTAAAACAATCATGATTCAAGCATTTACAACGACGA	762
OY	61 LysValAlaleutyryllealthmetelgsypnglnglyserylserleuthrnclygly 80	
Dd	763 AAAAGTGCATTGTATAATTGCACCTATGGGCGCACCAAAGGTTCAGGCAGTTTGACAGGGGGT	822
OY	81 ArgTySerilLeAspaAlaleuilleaRgLyguTyrlleasnSerPrOlaVataArghThr 100	
Dd	823 CGCTACTTCATTGATGACATGATTTGCCGCCGAATACATPAACAGCCCTGCCGACC	882
OY	101 AspyrthrtyrproargyrGLuThrhralaglurthrhserylglyleuthrnlly 120	
Dd	883 GATTACACCTATCCCGCTTAGAACAAACAACCGCTGAACAAACATCAGCGGTTGACGGGT	942
OY	121 LeunThrTrsrleuseSrThreuaSnllaProalaeseargrThrnIsertarsply 140	
Dd	943 TTAAACGACTCTTTATCTTACACTTATATCCCCCTGCAGCTCGCGCACCCATACACAGCGT	1002

QY	141	SeRGlySeRaRgSeSerLeuGlyLeuAsn11eGlyGlyMeGlyAspTYrARgAsnGlu	160
Db	1003	AGCGGAATGAGAGACAGTCTGGGCTTAAATATGTGGCGGAATGGGGGATTTATCGAAATGAA	1067
QY	161	ThrLeuThrTrtAsnProARgAspThrZalAheLeuSeSerhiSLeuValGlnThrValPhe	180
Db	1063	ACCTTGACGACCAACCCGGCGGACGCTCCITTTCTTCCACTTGGTGTAAGACGTAATTT	1122
QY	161	PheLeuArGgly11eAspValValSerProAlaAsn1aAspThrAspValPhe11eAsn	200
Db	1123	TTCTCGCCCGGCAATAGAGGTGTCTCTCCGCAATGCGCATGAGATGTTTAAATTAAAC	1182
QY	201	11eAspValPheGlyThr11eArgAsnArgThrGluMeChSLeuTYrAsn1aGlnThr	220
Db	1183	ATCGACGCTATTGAGACCATATCGCAACGAAACCGAAATGCACCTRTACATGCCGAAACA	1247
QY	221	LeuLYsAlaGlnThrLYeLeuGlnTYrPheAlaValAspArGThrAsnLYeLYeLeu	240
Db	1243	CTGAAGCCCAACAAACCTGAATATTCTCCAGTAGACAAACCAATATTAATAATTCCTC	1302
QY	241	11eLYsProLYsTrtAsnAlaPheGlnLYa1a1aTYrLYsGlnAsnTYrAlaLeuTrpMet	260
Db	1303	ATCAAAACCAAAACCAATGCGTTTGAACTGCTCTRTAAAGAAATTAACGCAATTGTGGATG	1362
QY	261	GlyProTYrLYsValSerLYsGly11eLYsProThrGlnGlyLeuMeValAspPheSer	280
Db	1363	GGGCGGTATTAAGTAGACAAAGAAATCAAAACCGACGGAAGGATTATATGTCGATTCCTC	1422
QY	281	Asp11eArGProTYrGlyLYsAsnhiEThrGlyAsnSerAlaProSeValGln1aAspAsn	300
Db	1423	GATATCCGGCCATACGGGAATCATACGGGTACTCCGCCCATCCGTAGAGGCTGATTAAC	1482
QY	301	SerhiGlnGlyTYrGlyTYrSerAspGln1aValArgGlnhiArgGlnGlyGlnPro	320
Db	1483	AGTCATGAGGGGTATGATATACAGCATTAACAGATGCGACAAACATATAGCAAGGGCAACT	1542
RESULT 2			
ABZ37917	ABZ37917 standard; DNA; 960 BP.		
ID	ABZ37917 standard; DNA; 960 BP.		
XX	ABZ37917;		
AC	07-MAR-2003 (first entry)		
DT	N. gonorrhoeae nucleotide sequence SEQ ID 423.		
DE	Antibacterial; infection; vaccine; gene therapy; gene; ds.		
XX	Neisseria gonorrhoeae.		
OS	Neisseria gonorrhoeae.		
XX	WO200279243-A2.		
FN	10-OCT-2002.		
XX	12-FEB-2002; 2002WO-IB002069.		
XX	12-FEB-2001; 2001GB-00003424.		
XX	(CHIR-) CHIRON SPA.		
XX	Fontana MR, Pizza M, Maignani V, Monaci E;		
XX	WPI; 2003-058415/05.		
DR	P-PSDB; ABP76947.		
XX	New protein from Neisseria gonorrhoeae, useful for the manufacture of a		
PT	medicament for treating or preventing N. gonorrhoeae infection.		
XX	Disclosure; Page 220; 815bp; English.		
XX	The present invention relates to proteins from Neisseria gonorrhoeae.		
CC	Also disclosed are the nucleic acid molecules encoding the proteins and		
CC	antibodies that specifically bind to the proteins. The composition		

CC completing the protein, nucleic acid or antibody is useful for the
 CC manufacture of a medicament for treating or preventing N. gonorrhoeae
 CC infection, this may be in the form of a vaccine or gene therapy.
 CC Sequences given in records AB237706-AB242016 represent nucleic acid
 CC molecules of the invention

XX Sequence 960 BP; 275 A; 241 C; 225 G; 219 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	2,57e-158	Length:	960
Score:	1641.00	Matches:	319
Percent Similarity:	100.00%	Conservative:	1
Best Local Similarity:	99.69%	Mismatches:	0
Query Match:	99.76%	Indels:	0
DB:	10	Gaps:	0

US-10-617-835-4 (1-320) x AB237917 (1-960)

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Oy 21 ThrLeuThnGlyIleProSerHisGlyGlyIlyValArgPheAlaValGluGlnGluLeu 40
Db 61 ACACGACAGCATATTCATCGCATGCGGAGCGCAACCGCTTCGCGGTGCAACAGACTT 120

Oy 41 ValAlaAlaSerAlaArgAlaAlaValIlyAspMetAspLeuGlnAlaLeuHisGlyArg 60
Db 121 GTGGCGCGCTTCGCGAGAGCTCGCTTAAAGACATGATTTACAGGCATTACACGACGA 180

Oy 61 LysValAlaLeuTyrlleAlaThrMetGlyAspGlnGlySerIleuThnGlyGly 80
Db 181 AAAGTTGCACTTGTACATTGCACTATGAGCGACAAAGTTGCGGAGTTGACAGGAGGT 240

Oy 81 ArgTyrSerIleAspAlaLeuIleArgGlyGlyTyrIleAsnSerProAlaValArgThr 100
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Oy 101 AspTyrThnTyrProArgTyrGluThrThralaGluThnThrSerGlyIleuThnGly 120
Db 301 GATTACACCTATCCCGTTACGAAACCAACCGCTGAAACAAATCAAGCGGTTGACGGGT 360

Oy 121 LeuThnThrSerLeuSerThrLeuAsnAlaProAlaLeuSerArgThnGlnSerAspGly 140
Db 361 TTAAACCACTCTTTTATCTACACTTAATGCCCCCTGCACTCTCGCGACCCAAATCAAGCGGT 420

Oy 141 SerGlySerArgSerSerLeuGlyLeuAsnIleGlyGlyMetGlyAspTyrArgAsnGlu 160
Db 421 AGCGGAAGTAGAGACAGCTGCGCTTAATATTGGCGGAGATGGGGGATTATCGAAATGA 480

Oy 161 ThrLeuThnThrAsnProArgAspThralaPheLeuSerHisLeuValGlnThrValPhe 180
Db 481 ACCTTGACGACCAACACCGCGGACACACTGCTTTCTTCCACTGTCGACGACCGATATT 540

Oy 181 PheLeuArgGlyIleAspValIleSerProAlaAsnAlaAspThnAspValPheIleAsn 200
Db 541 TTCCTGCGGCGCATAGAGCTGTCTCTCTCCAAATGCCGATACAGATGTGTTATTAAAC 600

Oy 201 IleAspValPheGlyThnIleArgAsnArgThnGluMetHisLeuTyrAsnAlaGluThn 220
Db 601 ATCGACGATATTGGAACGATACGCAACGAAACGAAATGCACTTATACATCCGAAACA 660

Oy 221 LeuLysAlaGlnThnLysLeuGluTyrPheAlaValAspArgThnAsnLysLeuLeu 240
Db 661 CTGAAGACCCCAACAACTGGAATATTTTCGACAGTAGACAGAACCAATMAAAATTTGCTCC 720

Oy 241 IleLysProLysThnAsnAlaPheGluAlaAlaTyrLysGluAsnTyrAlaLeuTyrMet 260
Db 721 ATCAAAACCAAAACCAATCGCTTTGAGCTGCTTAAAGAAATTAATCCATTGCGATG 780

Oy 261 GlyProTyrLysValSerIleGlyIleLysProThnGluGlyLeuMetValAspPheSer 280
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Oy 261 AspIleArgProTyrGlyAsnHisPheThrGlyAsnSerAlaProSerValGluAlaAspAsn 300
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Oy 301 SerHisGluGlyTyrGlyTyrSerAspGluAlaValaIaArgGlnHisArgGlnGlyGlnPro 320
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RESULT 3

AAZ12008
 ID AAZ12008 standard; DNA; 963 BP.

AC AAZ12008;

DT 08-OCT-1999 (first entry)

DE Neisseria gonorrhoeae complete ORF15 sequence.

KW Neisseria meningitidis; Neisseria gonorrhoeae; antigen; vaccine;
 KW treatment; Neisseria infection; meningitis; septicemia; gonorrhea; ss.

OS Neisseria gonorrhoeae.

PN W0924578-A2.

PD 20-MAY-1999.

PF 09-OCT-1998; 98WO-IB001665.

PR 06-NOV-1997; 97GB-00023516.

PR 14-NOV-1997; 97GB-00024190.

PR 18-NOV-1997; 97GB-00024386.

PR 27-NOV-1997; 97GB-00025158.

PR 10-DEC-1997; 97GB-00026147.

PR 14-JAN-1998; 98GB-00000759.

PR 01-SEP-1998; 98GB-00019016.

XX (CHIR-) CHIRON SPA.

XX Masignani V, Rappuoli R, Pizza M, Scarlato V, Grandi G;

XX WPI: 1999-327407/27.

XX P-PSDB; AAY38540.

XX Proteins from Neisseria meningitidis and N. gonorrhoeae useful for

XX diagnosis, treatment and prevention of infection.

XX Claim 9; Page 100; 524pp; English.

XX Nucleotide sequences AAZ11972-212358 represent open reading frames (ORFs)

XX of Neisseria meningitidis and N. gonorrhoeae which encode antigenic

XX proteins (see AAY38499-Y38944). The antigenic proteins, their fragments,

XX their nucleic acids and antibodies are used for diagnosis, prevention (as

XX vaccines) or treatment of Neisseria infections, such as meningitis,

XX septicemia and gonorrhea. Both organisms are closely related. Fragments

XX of the nucleic acids are useful as hybridisation probes and antisense

XX reagents

SQ Sequence 963 BP; 276 A; 241 C; 226 G; 220 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	2,58e-158	Length:	963
Score:	1641.00	Matches:	319
Percent Similarity:	100.00%	Conservative:	1
Best Local Similarity:	99.69%	Mismatches:	0
Query Match:	99.76%	Indels:	0
DB:	2	Gaps:	0

US-10-617-835-4 (1-320) x AAZ12008 (1-963)

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Oy 1 MetATGAlaArgLeuLeuIleProIleuPheSerValPheIleuSerAlaCysGly 20
  
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Db      1 ATGCGGACGCGCTGTGATACCTATCTTTTTCAGTTTATTTTATCCGCTCGCGG 60
Oy      21 ThrLeuThrGlyIleProSerHisGlyGlyValysArgPheAlaValGluGlnIleu 40
Db      61 ACACGACAGGGATTCACATCGCATGCGGAGCAAAACGCTTCGCGTGAACAACACTT 120
Oy      41 ValAlaAlaSerAlaArgAlaAlaValLysAspMetAspLeuGlnAlaLeuHisGlyArg 60
Db      121 GTGGCGGCTTGTGCGAGAGCTCCGTTAAAGCAATGATTTTACAGCATTTACACGAGCA 180
Oy      61 LysValAlaLeuTyrIleAlaThreMetGlyAspGlnGlySerGlySerLeuThrGlyGly 80
Db      181 AAAGTTGATGTGATTCATTCACATATGCGCGACCAAGGTTCCAGGCAAGTTTGACAGGGGGT 240
Oy      81 ArgTyrSerIleAspAlaLeuIleArgGlyGlyTyrIleAsnSerProAlaValArgThr 100
Db      241 CGCTCTCATTTGATGACCTGATTCGCGCGAATTCATTAACAGCCCTTCGCGTCCGCAACC 300
Oy      101 AspTyrThrTyrProArgTyrGlyuThrThrAlaGluThrThrSerGlyGlyLeuThrGly 120
Db      301 GATTACACCTATCCGCTTACGAACCAACCGCTGAACCAACATCATCGCGGTTTGAACGGGT 360
Oy      121 LeuThrThrSerLeuSerThrLeuAsnAlaProAlaLeuSerArgThrGlnSerAspGly 140
Db      361 TTAAACCATCTTCTTATCTTACACTTATATCCCTCGCACTTCGCGCAACCAATCAGACCGT 420
Oy      141 SerGlySerArgSerSerLeuGlyLeuAsnIleGlyGlyMetGlyAspTyrArgAsnGlu 160
Db      421 AGCGGAAGTACGACAGTCTGGGCTTAAATTTGGCGGAGTGGGGATTTATCGAAATGAA 480
Oy      161 ThrLeuThrThrAsnProArgAspThrAlaPheLeuSerHisLeuValGlnThrValPhe 180
Db      481 ACCTTGACGACCAACCGCGCGACACCTGCTTTTCCACTTGTTCGACAGCGTATTT 540
Oy      181 PheLeuArgGlyIleAspValValSerProAlaAsnAlaAspThrAspValPheIleAsn 200
Db      541 TTCCTGCGCGCAATAGAGTGTTCCTCTCCATAGCCGATACAGATGTGTTATTTAAC 600
Oy      201 IleAspValPheGlyThrIleArgAsnArgThrGluMetHisLeuTyrAsnAlaGluThr 220
Db      601 ATCGACGATTCGAGACGATACCGCAACGAAACCGAAATGCACTTATACAAATCGCAACA 660
Oy      221 LeuLysAlaGlnThrLysLeuGlyuThrPheAlaValAspArgThrAsnLysLeuLeu 240
Db      661 CTGAAGGCCCAAAACAAACCTGGAATATTTGCGACATGACAGAACCAATAAAAATTTGCTC 720
Oy      241 IleLysProLysThrAsnAlaPheGluAlaAlaTyrLysGlyuAsnTyrAlaLeuTyrMet 260
Db      721 ATCAAAACCAAAACCAATGCGTTGAAGCTCCCTATTAAGAAAAATTCGCAATTTGTGATG 780
Oy      261 GlyProTyrLysValSerLysGlyIleLysProThrGluGlyLeuMetValAspPheSer 280
Db      781 GGGCCGATTAAGTAAGCAAGAAAGAAATCAACCGAAGGAGATTGATGCTTTCTCC 840
Oy      281 AspIleArgProTyrGlyAsnHisThrGlyAsnSerAlaProSerValGluAlaAspAsn 300
Db      841 GATATCCAAACCATACCGGCAATCATACGGGTAACTCCGCCCATCGATGAGCGTGAATAC 900
Oy      301 SerIleGlyGlyTyrGlyTyrSerAspGluAlaValArgGlnHisGlyGlnPro 320
Db      901 AGTCATGAGGGGTATGATACAGCATGAACAGTGCACAACATAGACAGGGGCAACCT 960

```

RESULT 4

AAZ54614
AAZ54614 standard; DNA, 963 BP.

AC AAZ54614;

DT 15-SEP-2003 (revised)

DT 21-MAR-2000 (first entry)

DE Neisseria gonorrhoeae ORF 406 partial DNA sequence SEQ ID NO:3111.

XX

KW Neisseria meningitidis; Neisseria gonorrhoeae; antigen; vaccine;
KW antigenic; diagnosis; immunogenic; infection; meningitis; septicemia;
KW antibacterial; gene therapy; ds.

OS Neisseria gonorrhoeae.

PN W0957280-A2.

PD 11-NOV-1999.

XX 30-APR-1999; 99WO-US009346.

PR 01-MAY-1998; 98US-0083758P.

PR 31-JUL-1998; 98US-0094869P.

PR 02-SEP-1998; 98US-0098994P.

PR 02-SEP-1998; 98US-0099062P.

PR 09-OCT-1998; 98US-0103749P.

PR 09-OCT-1998; 98US-0103794P.

PR 09-OCT-1998; 98US-0103796P.

PR 25-FEB-1999; 99US-0121528P.

XX (CHIR) CHIRON CORP.

PA (GENO-) INST GENOMIC RES.

P1 Fraser C, Galeotti C, Grandi G, Hickey E, Maignani V, Mora M,
P1 Petersen J, Pizzo M, Rappuoli R, Ratti G, Scalato E, Scarselli M,
P1 Tettelin H, Venter JC,

DR WPI: 2000-062150/05.

XX P-PSDB; AAY75812.

PT Novel Neisserial polypeptides predicted to be useful antigens for
PT vaccines and diagnostics.

XX Example 1; Page 109; 1453BP; English.

XX AAZ53015 to AAZ54536, AAZ54577 to AAZ54615, and AAY74253 to AAY75941
XX represent novel Neisseria meningitis and N. gonorrhoeae polynucleotides
XX and polypeptides. AAZ54537 to AAZ54576 and AAZ54616 to AAZ5473 represent
XX PCR primers used in the exemplification of the present invention. The
XX polypeptides, the polynucleotides, antibodies and compositions of the
XX invention can be used as vaccines, as diagnostic reagents, and as
XX immunogenic compositions. The polypeptides can be used in the manufacture
XX of medicaments for treating or preventing infection due to Neisserial
XX bacteria (e.g. meningitis and septicemia), to detect the presence of
XX Neisseria bacteria, or to raise antibodies. They may also be used to
XX screen for agonists or antagonists, which may themselves have use as
XX antibacterial agents. The polynucleotides of the invention may also be
XX used in gene therapy protocols. (Updated on 15-SEP-2003 to standardise OS
XX field)

XX SQ Sequence 963 BP; 276 A; 241 C; 226 G; 220 T; 0 U; 0 Other;
XX

Alignment Scores:

Pred. No.: 2.58e-158 Length: 963

Score: 1641.00 Matches: 319

Percent Similarity: 100.00% Conservative: 1

Best Local Similarity: 99.69% Mismatches: 0

Query Match: 99.76% Indels: 0

DB: 3 Gaps: 0

US-10-617-835-4 (1-320) x AAZ54614 (1-963)

Oy 1 MetArgAlaArgLeuLeuIleProIleLeuPheSerValPheIleLeuSerAlaCysGly 20

Db 1 ATGCGGACGCGCTGTGATACCTATCTTTTTCAGTTTATTTTATTCGCGCGG 60

Oy 21 ThrLeuThrGlyIleProSerHisGlyGlyValysArgPheAlaValGluGlnIleu 40

Db 61 ACACGACAGGGATTCATTCATGCGCATGCGGAGCAAAACGCTTCGCGTGAACAACACTT 120

Oy 41 ValAlaAlaSerAlaArgAlaAlaValLysAspMetAspLeuGlnAlaLeuHisGlyArg 60

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Db      121 GTGGCGGCTTCTCCAGAGCTGCCGTTAAAGACATGATTTCACGCGAACA 180
Qy      61 LysValAlaLeuTyrIleAlaThrMetGlyAspGlnGlySerGlySerLeuThrGlyGly 80
Db      181 AAAGTTGATTTGATTCATTGCACTATGGCGGACCAAGGTTTCAGGCAAGTTTGACAGGGGGT 240
Qy      81 ArgTyrSerIleAspAlaLeuIleArgGlyGlyTyrIleAspSerProAlaValArgThr 100
Db      241 CGCTACCTCCATTGATGACATGATGCGGCGGAATACATTAACAGCCCTCGCTCGCACCC 300
Qy      101 AspTyrThrTyrProArgGlyIleuThrThrAlaGluThrThrSerGlyGlyLeuThrGly 120
Db      301 GATTACACTTATCCGCGTTACGAACACCCGCTGAACACACATCAGCGCGTTGACGGGT 360
Qy      121 LeuThrThrSerLeuSerThrLeuAlaAlaProAlaLeuSerArgThrGlnSerAspGly 140
Db      361 TTAAACCACTTCTTTTATCTACCTTATATGCCCCCTGCACCTCCGACCAACATCAGACGGT 420
Qy      141 SerGlySerArgSerSerLeuGlyLeuAlaIleGlyGlyMetGlyAspTyrArgGlnGly 160
Db      421 AGCGGAAGTGAAGAGAGCTGGGCTTAAATATGCGGGATGGGATTTATCGAAATGAA 480
Qy      161 ThrLeuThrThrAsnProArgAspThrAlaPheLeuSerHisLeuValGlnThrValPhe 180
Db      481 ACCTTGACGACCAACCCCGCGCACACTGCTTTCTTCCACTTGTTGTCAGACCGTATTT 540
Qy      181 PheLeuArgGlyIleAspValValSerProAlaAlaSerThrAspValPheIleAsn 200
Db      541 TTCCTGCGCGCATAGACGCTTCTTCTCCGCAATGCGCATACAGATGCTTTATTAAC 600
Qy      201 IleAspValPheGlyThrIleArgAsnArgThrGlyMetHisLeuThrAsnAlaGluThr 220
Db      601 ATCGACGATTTGCAACGATACGCAACAGAACCCGAATGACCTTATACATGCCAACA 660
Qy      221 LeuValAlaGlnThrIleLeuGlyIleuThrPheAlaValAspArgThrAsnIleLeuLeu 240
Db      661 CTGAAGGCCCAACAACTGGAATTTTTCGCGATGACAGAACCAATAAATAATTGGCTC 720
Qy      241 IleLysProLysThrAsnAlaPheGluAlaAlaIleTyrLysGluAsnTyrAlaLeuTrpMet 260
Db      721 ATCAAAACCAAAACCAATGCGTTGAGCTGCTTAAAGAAATATACCATTTGCGATG 780
Qy      261 GlyProTyrLysValSerIleGlyIleLysProThrGlnGlyLeuMetValAspPheSer 280
Db      781 GGGCCGATTAAGTAAGCAAAAGAAATCAAAACCGACGAAAGATGATGTCGATTTCTCC 840
Qy      281 AspIleArgProTyrGlyAsnHisThrGlyAsnSerAlaProSerValGluAlaAspAsn 300
Db      841 GATATCCAAACCATACGCGCATATACGGGTAACTCCGCCCATTCGCTAGAGGCTGATAAC 900
Qy      301 SerHisGlnGlyTyrGlyTyrSerAspGluAlaValArgGlnHisArgGlnGlyGlnPro 320
Db      901 AGTCATGAGGGGTATGATGATACGCGATGACAGCAGTGCAGCAACATAGACCAAGGGCAACT 960

```

RESULT 5
AA253688
ID AA253688 standard; DNA; 963 BP.

AA253688;
AC
XX 15-SEP-2003 (revised)
DT 21-MAR-2000 (first entry)
XX
DE Neisseria gonorrhoeae ORF 406 partial DNA sequence SEQ ID NO:1325.
XX
KW Neisseria meningitidis; Neisseria gonorrhoeae; antigen; vaccine;
KW antigenic; diagnosis; immunogenic; infection; meningitis; septicemia;
KW antibacterial; gene therapy; ds.
XX
OS Neisseria gonorrhoeae.
XX
PN W09957280-A2.
XX

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PD      11-NOV-1999.
XX
PF      30-APR-1999; 99WO-US009346.
XX
PR      01-MAY-1998; 98US-0083758P.
XX      31-JUL-1998; 98US-0094869P.
PR      02-SEP-1998; 98US-0098994P.
PR      02-SEP-1998; 98US-0099062P.
PR      09-OCT-1998; 98US-0103749P.
PR      09-OCT-1998; 98US-0103794P.
PR      09-OCT-1998; 98US-0103796P.
PR      25-FEB-1999; 99US-0121528P.
XX
PA      (CHIR) CHIRON CORP.
PA      (GENO-) INST GENOMIC RES.
XX
PI      Fraser C, Galeotti C, Grandi G, Hickey E, Maignani V, Mora M;
PI      Petersen J, Pizzi M, Rappuoli R, Ratti G, Scalato E, Scarselli M;
PI      Tettelin H, Venter JC;
DR      WPI, 2000-062150/05.
DR      P-PsDB: AAY74926.
XX
PT      Novel Neisserial polypeptides predicted to be useful antigens for
PT      vaccines and diagnostics.
XX
PS      Claim 7, Page 728, 1453pp; English.
XX
CC      AA253015 to AA254536, AA254577 to AA254615, and AAY74253 to AAY75941
CC      represent novel Neisseria meningitidis and N. gonorrhoeae polynucleotides
CC      and polypeptides; AA254537 to AA254576 and AA254616 to AA254673 represent
CC      PCR primers used in the exemplification of the present invention. The
CC      polypeptides, the polynucleotides, antibodies and compositions of the
CC      invention can be used as vaccines, as diagnostic reagents, and as
CC      immunogenic compositions. The polypeptides can be used in the manufacture
CC      of medicaments for treating or preventing infection due to Neisserial
CC      bacteria (e.g. meningitis and septicemia), to detect the presence of
CC      Neisseria bacteria, or to raise antibodies. They may also be used to
CC      screen for agonists or antagonists, which may themselves have use as
CC      antibacterial agents. The polynucleotides of the invention may also be
CC      used in gene therapy protocols. (Updated on 15-SEP-2003 to standardise OS
CC      field)
XX
SQ      Sequence 963 BP; 276 A; 241 C; 226 G; 220 T; 0 U; 0 Other;

```

Alignment Scores:

Pred. No.: 2,598-158 Length: 963
 Score: 1641.00 Matches: 319
 Percent Similarity: 100.00% Conservative: 1
 Best Local Similarity: 99.69% Mismatches: 0
 Query Match: 99.76% Indels: 0
 DB: 3 Gaps: 0

US-10-617-835-4 (1-320) x AA253688 (1-963)

```

Qy      1 MetArgAlaArgLeuIleProIleuPheSerValPheIleLeuSerAlaCysGly 20
Db      1 ATGGGGGACGGCTGCTGATACCTATCTTTTTCAGTTTATTTATTCGCCCTGGCGGG 60
Qy      21 ThrLeuThrGlyIleProSerHisGlyGlyGlyLysArgPheAlaValGlnGlnLeu 40
Db      61 ACACGACAGATTTCCATCCGATGCGGACGAGCAAAACCTTCGCGCTGACACAGAACTT 120
Qy      41 ValAlaAlaSerAlaArgAlaAlaValAlaAspMetAspLeuGlnAlaLeuHisGlyArg 60
Db      121 GTGGCGGCTTCTGCGACAGCTGCGGTTAAACATGATGATTTACAGGCACTTACACCGAGCA 180
Qy      61 LysValAlaLeuTyrIleAlaThrMetGlyAspGlnGlySerGlySerLeuThrGlyGly 80
Db      181 AAAGTTGATTTGATTCATTGCACTATGCGGCAACAGGTTTCAGGCGATTTGACAGGGGGT 240
Qy      81 ArgTyrSerIleAspAlaLeuIleArgGlyGlyIleuThrThrAlaGluThrThrSerProAlaValArgThr 100

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Db 241 CGTACTCATTCATGATGACGATTCGGCGGCAATACATAAACGCCCTGCCGACC 300
Qy 101 AspTYrThrTYrProArgTYrGluThrThraAlaGluThrThrSerGlyGlyLeuThrGly 120
Db 301 GATTACACCTTATCCGCGGTACGAAACACCCCTGAAACAAATCAAGGGGTTTACGCGGT 360
Qy 121 LeuThrThrSerLeuSerThrIleuAsnAlaProAlaLeuSerArgThrGlySerAspGly 140
Db 361 TTAACCACTTCTTATCTACACTTAATCCCTGACTCTGGCGACCACTACAGCGGT 420
Qy 141 SerGlySerArgSerSerLeuGlyLeuAsnIleGlyIleMetGlyAspTYrArgAsnGlu 160
Db 421 AGCGGAAGTAGAGAGAGCTGGGCTTAATATTTGGCGGAGATGGGGGATTATCGAAATGAA 480
Qy 161 ThrLeuThrThrAsnProArgAspThrAlaPheLeuSerThrIleuValGluThrValPhe 180
Db 481 ACCTTGAGACCAACCCGCGGACACTCCCTTCTTCCACTGGTGTCAGACCGTATTT 540
Qy 181 PheLeuArgGlyIleAspValValSerProAlaAsnAlaAspThrAspValPheIleAsn 200
Db 541 TTCTCGCGCGCATGACGTTGTTCTCTCGCAATGCGATACAGATGTGTTATTATAC 600
Qy 201 IleAspValPheGlyThrIleArgAsnArgThrGluMetIleLeuTYrAsnAlaGluThr 220
Db 601 ATCGACGATTCGGGAACGATACGCAACCAACCGAAATGCACTATACAAATGCCGAAACA 660
Qy 221 LeuIysAlaGluThrIleuLeuGluThrPheAlaValAspArgThrAsnIleuLeu 240
Db 661 CTGAAGGCCCAACCAAACTGAAATATTTCCAGTAGCAAGAACCAATTAATAATTTGCTC 720
Qy 241 IleIysProIysThrAsnAlaPheGluAlaIleAlaTYrIleGlyAsnTYrAlaLeuTYrMet 260
Db 721 ATCAAAACCAAAACCAATGCGTTTGAACCTGCTATAAAGAAATTAACGCAATTGGCATG 780
Qy 261 GlyProTYrIysValSerIleGlyIleIysProThrGluGlyLeuMetValAspPheSer 280
Db 781 GGGCGCATTAAGTAAGCAAGAAAGATCAAAACCGAAGGATTCGATGCTGCTCC 840
Qy 281 AspIleArgProTYrGlyAsnHisThrGlyAsnSerAlaProSerValGluAlaAspAsn 300
Db 841 GATATCCACCATACGCGCATATCATACGGGTAACTCCGCCCATCCGTAGAGGCTGATAC 900
Qy 301 SerHisGluGlyTYrGlyTYrSerAspGluAlaValAlaArgIleHisArgGluGlyPro 320
Db 901 AGTCATGAGGGGTATGATACAGCATGACGATGACGACAACTATGACAAAGGCAACT 960
RESULT 6
AAAB1297
ID AAAB1297 standard; DNA; 963 BP.
XX
XX AAA81297;
XX
XX 15-SEP-2003 (revised)
XX 04-DEC-2000 (first entry)
XX
DE N. gonorrhoeae partial DNA sequence g406.seq SEQ ID NO:1036.
XX
XX Neisseria meningitidis; Neisseria gonorrhoeae; genome; immunogenic;
XX antigen; vaccine; diagnosis; infection; antibacterial; identification;
XX Meningococcus B; MenB; ds.
XX
XX Neisseria gonorrhoeae.
XX
XX MO200022430-A2.
XX
XX 20-APR-2000.
XX
XX 08-OCT-1999; 99WO-US023573.
XX
XX 09-OCT-1998; 98US-0103794P.
XX 30-APR-1999; 99US-0132068P.
XX
XX (CHIR ) CHIRON CORP.
PA

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XX
PI Frazer CM, Hickey B, Peterson J, Terteljn H, Venter JC;
PI Maignani V, Galeotti C, Mora M, Ratti G, Scarselli M, Scarlato V;
PI Rappuoli R, Pizza M;
XX
XX WPI; 2000-318079/27.
DR P-PSDB; AAB25657.
XX
XX Isolated nucleotide sequences of Neisseria meningitidis which can be used
PT in the diagnosis and treatment of N. meningitidis infection and other
PT Neisserial infections, for example, N.gonorrhoea.
XX
XX Claim 9; Page 108; 1760pp; English.
XX
XX The present invention describes methods of obtaining immunogenic proteins
CC from Neisseria genomic sequences. AAAB1453 to AAAB2414 represent
CC specifically claimed Neisseria meningitidis genomic DNA sequences;
CC AAAB1260 to AAAB1303 and AAB25620 to AAB25663 represent Neisseria DNA
CC sequences and their corresponding proteins; AAAB1254 to AAAB1259 and
CC AAAB1304 to AAAB1321 represent PCR primers used in the isolation of
CC Neisseria meningitidis DNA sequences; and AAAB1322 to AAAB1452 represent
CC Neisseria meningitidis MenB polynucleotide ORF sequences, which are all
CC used in the exemplification of the present invention. The nucleic acid
CC sequences, protein sequences, and antibodies against them, can be used in
CC the manufacture of a composition. The composition can be used as a
CC medicament (or in the manufacture of a medicament) for treating,
CC preventing or diagnosing infection due to Neisserial bacteria. For
CC example, some of the identified proteins could be components of vaccines
CC against Meningococcus B; against all serotypes; and/or against all
CC pathogenic Neisseriae. Identification of sequences from the bacterium
CC will also facilitate production of biological probes, particularly
CC organism-specific probes. Attempts to make efficacious Meningococcus B
CC vaccines have failed mainly due to antigen tolerance. Multivalent
CC vaccines have also been tried but none have successfully overcome
CC antigenic variability. The provision of further, complete sequences may
CC provide an opportunity to identify secreted or surface exposed proteins
CC that may be presumed targets for the immune system and which are not
CC antigenically variable or at least more conserved than other more
CC variable regions. (Updated on 15-SEP-2003 to standardise OS field)
XX
XX
SQ Sequence 963 BP; 276 A; 241 C; 226 G; 220 T; 0 U; 0 Other;
XX
Alignment Scores:
Pred. No.: 2,58e-158 Length: 963
Score: 1641.00 Matches: 319
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 99.69% Mismatches: 0
Query Match: 99.76% Indels: 0
DB: Gaps: 3
XX
US-10-617-835-4 (1-320) x AAA81297 (1-963)
Qy 1 MetArgAlaArgLeuLeuIleProIleLeuPheSerValPheIleLeuSerAlaCysGly 20
Db 1 ATGCGGGACAGCGCTGCGATACCTATCTTTTCAGTTTATTATTATCCGCTCGGG 60
Qy 21 ThrLeuThrGlyIleProSerHisGlyGlyIleIysArgPheAlaValGluGluLeu 40
Db 61 ACACTGACAGGTATTCATGCGCATGCGGAGGCAAAAGCTTCGGGTCGAACAAAGAACTT 120
Qy 41 ValAlaAsnSerAlaArgAlaAlaValIleAspMetAspLeuGluAlaLeuHisGlyArg 60
Db 121 GTGGCCGCTTCTGCAAGAGCTGCCGTAAAGACATGATTTACAGGCAATTACAGGACGA 180
Qy 61 LysValAlaLeuTYrIleAlaThrMetGlyAspGluGlySerGlySerLeuThrGlyGly 80
Db 181 AAAGTTCATTTGATGACATGCACTATGGGCGACCAAGATTCAGGCACTTTGACAGGGGCT 240
Qy 81 ArgTYrSerIleAspAlaLeuIleArgGlyGluTYrIleAsnSerProAlaValArgThr 100
Db 241 CGTACTCATTCATGATGACGATTCGGGCGGAATACATTAACACCCCTGCCGTCGCAACC 300
Qy 101 AspTYrThrTYrProArgTYrGluThrThraAlaGluThrThrSerGlyGlyLeuThrGly 120

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Db      301 GATTACCACTATCCGGGTTACGAAACCAACCGCTGAAACATCATCAGCCGGTTGACGGGT 360
Oy      121 LeuThrThrSerLeuSerThrLeuAana1aPro1aLeuSerArgThrGlnSerAepGly 140
Db      361 TTACACACTCTTTATCTACCTAATATGCCCTGCACTCCGGGCAACCCCAATGACAGCGGT 420
Oy      141 SerGlySerArgSerLeuGlyLeuAan11eglyGlyMetGlyAepThyArgAanglu 160
Db      421 ACCGGAGAGAGGCGCTGGCTTAAATATGCGGAGATGGGGGATTAATCAAAATGAA 480
Oy      161 ThrLeuThrThrAspProArgAepThra1aPheLeuSerHisLeuValGlnThrValPhe 180
Db      481 ACCTTACACACCAACCCGCGGCACTGCTTTCTTCCACTGGTGGACACCGATATTT 540
Oy      181 PheLeuArgGly11eAspVal1aSerPro1aAana1aAspThraPval1Phe1eAan 200
Db      541 TTCCTGCGGGCATACCGTTGTTCTCTGCGCAATGCCGATACAGATGTTATTAAC 600
Oy      201 11eAspVal1PheGlyThr11eArgAana1gThrGlnMetHisLeuThyArgAan1aGluThr 220
Db      601 ATCGACGATTCGGAAACGATACGCAACAGAACCGAAATGCACTATACATGCGCAAAACA 660
Oy      221 LeuValA1aG11Thr1eLeuGluThyPheA1aVal1aAspArgThra1a1eAsp1eLeu 240
Db      661 CTGAAAGCCCAACAACTGCAATTTTCGCACTGACACACCAATTAATAAATTGCTC 720
Oy      241 11eAspPro1eThra1a1aPheGlu1a1a1a1eAsp1eLeu1a1eAsp1eLeu1a1eAsp1e 260
Db      721 ATCAAAACCAAAACCAATCGTTGAAAGCTGCTATTAAGAAATTAACCATTTGTGAG 780
Oy      261 GlyProThy1eVal1eSer1eGly11eAspProTh1eGly1eLeuMetVal1eAsp1eSer 280
Db      781 GGGCGGTATTAAGTAAAGCAAGCAACCAACCGAAGGATGATGATGATGATGATGATG 840
Oy      281 Asp1eAspProThy1eAsp1eThra1eAsp1eThra1eAsp1eThra1eAsp1eThra1eAsp 300
Db      841 GATATTCACACATACGCGCATCATCAGGTAATCTCCGCCCATCGCTAAGGCTGATTAAC 900
Oy      301 SerHisGluGly1eThy1eThySerAepGlu1a1aVal1aGlnHisArgGln1eGlnPro 320
Db      901 AGTCATGAGGGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 960
RESULT 7
AAAF21582
ID      AAF21582 standard; DNA; 963 BP.
XX
XX      AAF21582;
AC      15-SEP-2003 (revised)
XX      DT      13-MAR-2001 (first entry)
XX      DE      N. gonorrhoeae partial DNA sequence g406.seq SEQ ID NO.76.
XX      KM      Neisseria meningitidis; Neisseria gonorrhoeae; immunogenic; vaccine;
XX      KM      diagnosis; antigen; detection; infection; gene therapy; antibacterial;
XX      KM      ds.
XX      OS      Neisseria gonorrhoeae.
XX      PN      WO200066791-A1.
XX      PD      09-NOV-2000.
XX      PF      08-MAR-2000; 2000WO-US005928.
XX      PR      30-APR-1999; 99US-0132068P.
XX      PR      08-OCT-1999; 99WO-US023573.
XX      PR      28-FEB-2000; 2000GB-00004695.
XX      PA      (CHIR ) CHIRON CORP.
XX      PA      (GENO-) INST GENOMIC RES.

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PI      Pizza M, Hickey E, Peterson J, Tetrelin H, Venter JC;
PI      Massignani V, Galeotti C, Mora M, Ratti G, Scarselli M, Scariato V;
PI      Rappelli R, Frazer CM, Grandi G;
XX      WPI; 2000-647603/62.
DR      P-PSDB; AAB58587.
XX      Neisseria meningitidis B full length genome sequence and open reading
PT      frames are used to detect, treat and prevent Neisserial infections.
XX      Example 1; Page 109; 692pp; English.
XX      The present invention describes the full length genome of Neisseria
CC      meningitidis B (NMB). The sequences in AAF21544 and AAF21607 to AAF21613
CC      represent fragments of the NMB genomic sequence, as the sequence was too
CC      long to go in a record on its own it was split into 8 sequences which
CC      overlap each other at the beginning and end of each sequence by 49980 bp
CC      (i.e. the last 49980 bp of AAF21544 is repeated at the beginning of
CC      AAF21607, the last 49980 bp of AAF21607 are repeated at the beginning of
CC      AAF21608, and so on). AAF21545 to AAF21588 encode the Neisseria proteins
CC      given in AAB58550 to AAB58593, and AAF21589 to AAF21606 represent PCR
CC      primers which are used in the exemplification of the present invention.
CC      The NMB genome and fragments from it have antibacterial activity, and can
CC      be used in vaccines and gene therapy. Neisseria nucleic acids, proteins
CC      and/or antibodies which binds to the proteins can be used in compositions
CC      for treating or preventing infection due to Neisserial bacteria or as a
CC      diagnostic reagent for detecting the presence of Neisserial bacteria or
CC      of antibodies raised to Neisserial bacteria. Computers, computer memory,
CC      computer storage medium or computer databases can be used in a search to
CC      identify open reading frames (ORFs) or coding sequences within the NMB
CC      genome. The DNA sequences provide further opportunities to find antigenic
CC      or immunogenic proteins which are more effective in vaccines than the
CC      outer membrane proteins currently used. (Updated on 15-SEP-2003 to
XX      standardise OS field)
XX      SQ      Sequence 963 BP; 276 A; 241 C; 226 G; 220 T; 0 U; 0 Other;
XX
XX      Alignment Scores:
XX      Pred. No.: 2,586-158
XX      Score: 1641.00 Length: 963
XX      Percent Similarity: 100.00% Matches: 319
XX      Best Local Similarity: 99.69% Mismatches: 1
XX      Query Match: 99.76% Indels: 0
XX      DB: 3 Gaps: 0
XX
XX      US-10-617-835-4 (1-320) x AAF21582 (1-963)
Oy      1 MetArgAlaArgLeuLeu1ePro1eLeuPheSerValPhe1eLeuSer1aCysGly 20
Db      1 ATCGGGGACGCGCTGCTGATTAATCTTTTTCAGTTTATTTATTCCTCCGCGGG 60
Oy      21 ThrLeuThrGly1eProSerHisGlyGly1eAspPhe1aVal1eGlnGlnLeu 40
Db      61 ACATGACAGGATTCATCCATCGCATGCGGAGCAACCGCTGCGGTGCMAACAACACTT 120
Oy      41 Val1a1a1aSer1a1aArg1a1a1aVal1eAspMetAapLeuGln1eLeu1eGlyArg 60
Db      121 GTGGCCGCTTCGCGAGAGCTGCGTTAAAGCAATGATTTACAGCATTTACAGACCA 180
Oy      61 LysVal1a1eLeuThy1eAla1aThreGlyAepGln1eSerGlySerLeuThrGly 80
Db      181 AAAGTTGATTTGATTCATGCACTATGGCGACCAAGTTCAGCGATTTGACAGGGGT 240
Oy      81 ArgTySer1eAsp1aLeu1eArgGlyThy1eAspSerPro1aVal1aArgThr 100
Db      241 CGCTACTCCATTCATGATGACATGATTCGCGCGAATCATTAACAGCCCTGCCCGCAC 300
Oy      101 AspTyThrThyProArgTyGluThrThra1aGluThrThrSerGlyGlyLeuThrGly 120
Db      301 GATTACACCTATCCGCTTACAAACCAACCGCTGAACCAATCAGCGCGTTGACGGGT 360
Oy      121 LeuThrThrSerLeuSerThrLeuAana1aPro1aLeuSerArgThrGlnSerAepGly 140

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Db      361  TTAACCACTTCTTACTACTTAATGCCCCCTGCACTCTCCGCGACCCCAATCAGACGGT
Qy      141  SerGlySerArgSerSerLeuGlyLeuAsnIleGlyGlyMetGlyAspThrArgAsnGlu
Db      421  AGCGGAAGAGAGAGAGCTGGGCTTAATTTGGGGATGGGATATATGAAATGAA
Qy      161  ThrLeuThrThrAsnProArgAspThrAlaPheLeuSerHisLeuValGlnThrValPhe
Db      481  ACCTTGACGACCAACCCCGCGACACTGGCTTTCTTTCCCACTTGTGTGACACCGTATTT
Qy      481  PheLeuArgGlyIleAspValValSerProAlaAsnAlaAspThrAspValPheIleAsn
Db      541  TTCCGCGCGCGCATGACGTTGTTCTCTCTGCCAATGCCGATACAGATGTTTATTAC
Qy      201  IleAspValPheGlyThrIleArgAsnArgThrGluMetHisLeuThrAsnAlaGluThr
Db      601  ATCGACGATTTGGAAACGATACGCAACGAAACCGAAATGCACTTATCAATGCCAAACA
Qy      221  LeuIysAlaGlnThrIlyLeuGluIuTyrrPheAlaValAspArgThrAsnIlyLeuLeu
Db      661  CTGAAGCCCAAAACAATCTGGAATATTTCCGAGTAGACAGAACCAATTAATAATTTGCTC
Qy      241  IleIysProIySerThrAsnAlaPheGluAlaAlaIlyIlyGlyAsnTyrAlaLeuTyrMet
Db      721  ATCAAAACCCAAACCAATGCGTTTGAAGCTGCTTAAAGAAATTAACGCAATGTGGATG
Qy      261  GlyProTyrIlyValSerIlyGlyIleIysProThrGluIlyLeuMetValAspPheSer
Db      781  GGGCGGTAAAGTAAAGCAAGAGAAATCAAAACCGAGAGAAATTAATGTCATTTCTTCC
Qy      281  AspIleArgProTyrGlyIlyAsnHisThrGlyIlyAsnSerAlaProSerValGluAlaAspAsn
Db      841  GATATCCAAACCATACGCGCAATCATACGGGTAACTCCGCCCATTCGTAGAGCGTATAC
Qy      301  SerHisGluGlyTyrGlyIlySerAspGluAlaValAlaArgGlnHisArgGlnGlyGlnPro
Db      901  AGTCATGAGGGGTATGATACAGCGATGAAAGCAATGACCAACATATGACAAAGGGCAACT
RESULT 8
AAZ12006
ID      AAZ12006 standard; DNA, 963 BP.
AC      AAZ12006;
DT      08-OCT-1999 (first entry)
XX      DE      Neisseria meningitidis strain B complete ORF15 sequence.
XX      KW      Neisseria meningitidis; Neisseria gonorrhoeae; antigen; vaccine;
XX      KW      treatment; Neisseria infection; meningitis; septicemia; gonorrhea; ss.
XX      OS      Neisseria meningitidis.
XX      PN      W09924578-A2.
XX      PD      20-MAY-1999.
XX      PE      09-OCT-1998; 98W0-IB001665.
XX      PR      06-NOV-1997; 97GB-00023516.
XX      PR      14-NOV-1997; 97GB-00024190.
XX      PR      18-NOV-1997; 97GB-00024386.
XX      PR      27-NOV-1997; 97GB-00025158.
XX      PR      10-DEC-1997; 97GB-00026147.
XX      PR      14-JAN-1998; 98GB-00000759.
XX      PR      01-SEP-1998; 98GB-00019016.
XX      PA      (CHIR-) CHIRON SPA.
XX      PI      Masignani V, Rappuoli R, Pizza M, Scarlato V, Grandi G;
XX      WP1; 1999-327407/27.
XX      DR      P-PSDB; AAY38538.

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XX      PT      Proteins from Neisseria meningitidis and N. gonorrhoeae useful for
XX      PT      diagnosis, treatment and prevention of infection.
XX      PS      Claim 9; Page 98; 524pp; English.
XX      CC      Nucleotide sequences AAZ11972-212358 represent open reading frames (ORFs)
XX      CC      of Neisseria meningitidis and N. gonorrhoeae which encode antigenic
XX      CC      proteins (see AAY38499-Y38944). The antigenic proteins, their fragments,
XX      CC      their nucleic acids and antibodies are used for diagnosis, prevention (as
XX      CC      vaccines) or treatment of Neisseria infections, such as meningitis,
XX      CC      septicemia and gonorrhea. Both organisms are closely related. Fragments
XX      CC      of the nucleic acids are useful as hybridisation probes and antisense
XX      CC      reagents
XX      SQ      Sequence 963 BP; 284 A; 234 C; 217 G; 228 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:      1,34e-157      Length:      963
Score:          1634.00      Matches:      317
Percent Similarity: 99.69%      Conservative: 2
Best Local Similarity: 99.06%      Mismatches: 1
Query Match:    99.33%      Indels:      0
DB:             2             Gaps:        0

US-10-617-835-4 (1-320) x AAZ12006 (1-963)
Qy      1      MetArgAlaArgLeuLeuIleProIleLeuPheSerValPheIleLeuSerAlaCysGly 20
Db      1      ATGCAAGACGCGCGTGGATACCTATTTCTTTTCAGTTTATTTATTCGCGCTCGCGG 60
Qy      21      ThrLeuThrGlyIleProSerHisGlyGlyIlyIysArgPheAlaValGluGlnGluLeu 40
Db      61      ACATGACAGGTATTCATCGCATGCGATGGCGAGGTAAACGCTTTGGCGTGAACAAAGACTT 120
Qy      41      ValAlaAlaSerAlaArgAlaAlaValIlyPheAspPheCysLeuGlnAlaLeuHisGlyArg 60
Db      121      GTGGCGCTTCTGCGACAGCGTCCGTTAAAGACATGATTTTACAGGCATTAACAGGACGA 180
Qy      61      LysValAlaLeuTyrIleAlaThrMetGlyAspGlnGlySerGlySerLeuThrGlyGly 80
Db      181      AAGTTGATTTGATGATGCTGCTACCTATGCGGACCAAGAGTTCAGGCAATTTGACAGGGGGT 240
Qy      81      ArgTyrSerIleAspAlaLeuIleArgGlyGluTyrIleAsnSerProAlaValArgThr 100
Db      241      CGTACTCCATTTGATGATGATGATTCGTGGCAATATCAATAAACAGCCCTGCGTCAACC 300
Qy      101      AspTyrThrTyrProArgTyrGluThrThrAlaGluThrThrSerGlyGlyLeuThrGly 120
Db      301      GATTACACCTATCCACCGTTACGAAACACCGCTGAAACAACATCATGCGGCTTACACAGT 360
Qy      121      LeuThrThrSerLeuSerThrIleuAsnAlaProAlaLeuSerArgThrGlnSerAspGly 140
Db      361      TTAACCACTTCTTACTACTTAATGCCCCCTGCACTCTCCGCGACCCCAATCAGACGGT 420
Qy      141      SerGlySerArgSerSerLeuGlyLeuAsnIleGlyGlyMetGlyAspTyrArgAsnGlu 160
Db      421      AGCGGAAGTAAAGCACTCGGGCTTAATTTGGGGATGGGATATATGAAATGAA 480
Qy      161      ThrLeuThrThrAsnProArgAspThrAlaPheLeuSerHisLeuValGlnThrValPhe 180
Db      481      ACCTTGACGACCTAACCCCGCGACACTGGCTTTCTTTCCCACTTGTGTGACACCGTATTT 540
Qy      181      PheLeuArgGlyIleAspValValSerProAlaAsnAlaAspThrAspValPheIleAsn 200
Db      541      TTCCGCGCGCGCATGACGTTGTTCTCTCTGCCAATGCCGATACAGATGTTTATTAC 600
Qy      201      IleAspValPheGlyThrIleArgAsnArgThrGluMetHisLeuThrAsnAlaGluThr 220
Db      601      ATCGACGATTTGGAAACGATACGCAACGAAACCGAAATGCACTTATCAATGCCAAACA 660
Qy      221      LeuIysAlaGlnThrIlyLeuGluIuTyrrPheAlaValAspArgThrAsnIlyGlyLeuLeu 240

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Db 661 CTGAAGCCCAACAACTGATATTTCCGACGTAGACAGAACCAATATAAATTGCTC 720
Qy 241 IleyPProLySThrAsnAlaPheGluAlaAlaIYrlyGluAsnTYrAlaLeuTrpMet 260
Db 721 ATCAACCAAAACCAATGCGTTGAGCTGCTTAAAGAAATTACGCAATTGGATG 780
Qy 261 GYProTYrlyValSerlyGlyIYrlySerProThrgluGluLeuMetValAspPheSer 280
Db 781 GGGCGGTATAAGTAAGCAAGAAATTAACCGACGAAAGATTAATGTCGATTTCTCC 840
Qy 281 AspIleAspProTYrGlyAsnIleThrgIyAsnSerAlaProSerValGluAlaAspAsn 300
Db 841 GATATCCGACCACTAGCGCAATCATACGGGTAACTCCGCCCATCCGTAGAGGCTGATAAC 900
Qy 301 SerHisGluGlyTYrGlyTYrlySerAspGluAlaValAlaTrgGluHisArgGlnGlyInPro 320
Db 901 AGTCATGAGGGGTATGATGATACAGCATGAAATGATGCGCAACAATAGACAAAGCAACT 960
RESULT 9
AA253689
ID AA253689 standard; DNA, 963 BP.
XX
AC AA253689;
XX
DT 21-MAR-2000 (first entry)
XX
DE Neisseria meningitidis ORF 406 partial DNA sequence SEQ ID NO:1327.
XX
KW Neisseria meningitidis; Neisseria gonorrhoeae; antigen; vaccine;
KV antigenic; diagnosis; immunogenic; infection; meningitis; septicemia;
KW antibacterial; gene therapy; de.
XX
OS Neisseria meningitidis.
XX
FN MO9957280-A2.
XX
PD 11-NOV-1999.
XX
XX 30-APR-1999; 99WO-US009346.
XX
FP 01-MAY-1998; 98US-0083758P.
PR 31-JUL-1998; 98US-0094869P.
PR 02-SEP-1998; 98US-0098994P.
PR 02-SEP-1998; 98US-0099062P.
PR 09-OCT-1998; 98US-0103794P.
PR 09-OCT-1998; 98US-0103794P.
PR 09-OCT-1998; 98US-0103796P.
PR 25-FEB-1999; 99US-0121528P.
XX
PA (CHIR) CHIRON CORP.
PA (GENO-) INST GENOMIC RES.
XX
PI Frazier C, Galeotti C, Grandi G, Hickey E, Masignani V, Mora M;
PI Petersen J, Piza M, Rappuoli R, Ratti G, Scalato E, Scarcella M;
PI Tettelin H, Veneri JC.
XX
XX WPI: 2000-062150/05.
DR P-PSDB; AAY74927.
XX
PT Novel Neisserial polypeptides predicted to be useful antigens for
PT vaccines and diagnostics.
XX
XX Claim 7; Page 728; 1453pp; English.
XX
CC AA253015 to AA254536, AA254577 to AA254615, and AAY74253 to AAY75941
CC represent novel Neisseria meningitis and N. gonorrhoeae polynucleotides
CC and polypeptides. AA254537 to AA254576 and AA254616 to AA255473 represent
CC PCR primers used in the exemplification of the present invention. The
CC polypeptides, the polynucleotides, antibodies and compositions of the
CC invention can be used as vaccines, as diagnostic reagents, and as
CC immunogenic compositions. The polypeptides can be used in the manufacture
CC of medicaments for treating or preventing infection due to Neisserial
CC bacteria (e.g. meningitis and septicemia), to detect the presence of

CC Neisseria bacteria, or to raise antibodies. They may also be used to
CC screen for agonists or antagonists, which may themselves have use as
CC antibacterial agents. The polynucleotides of the invention may also be
CC used in gene therapy protocols
SQ Sequence 963 BP; 284 A; 234 C; 217 G; 228 T; 0 U; 0 Other;
Alignment Scores:
Pred. No.: 1,346-157 Length: 963
Score: 1634.00 Matches: 317
Percent Similarity: 99.69% Conservative: 2
Best Local Similarity: 99.06% Mismatches: 1
Query Match: 99.33% Indels: 0
Gaps: 0
US-10-617-835-4 (1-320) x AA253689 (1-963)
Qy 1 MetArgAlaArgLeuLeuIleProIleLeuPheSerValPheIleLeuSerAlaCysGly 20
Db 1 ATGCAAGCAGCGCTGCTGCTGATACCTATCTTTTTCAGTTTTTATTTATCCGCTGCGG 60
Qy 21 ThrLeuThrgIyIleProSerHisGlyGlyIYrlyAspPheAlaValGluGlnGluLeu 40
Db 61 AACAGCAGAGGATTCATTCGATGCGGAGGTAAACCTTTGGCGTGAACAAGACTT 120
Qy 41 ValAlaAlaSerAlaArgAlaAlaValIyAspMetAspLeuGluAlaLeuHisGlyArg 60
Db 121 GTGGCGGCTCTGCGCAGAGCTGCCCTTAAAGCAATGATTTACAGCACTTACACGAGCA 180
Qy 61 LysValAlaLeuTYrIleAlaThreGlyAspGlnGlySerGlySerLeuThrgIyGly 80
Db 181 AAGTTGCAATGTACATTGCACTTGTGGCGACGACGTTTACAGGAGTTTGACAGGGGCT 240
Qy 81 ArgTYrSerIleAspAlaLeuIleArgIyGluTYrIleAsnSerProAlaValArgThr 100
Db 241 CGTACTCCATTTGATGACAGTGAATTCGTGGCGAATCATTAACAGCCCTGCGCTGACC 300
Qy 101 AspTYrThrTYrProArgTYrGluThrThralaGluThrThrSerGlyLeuThrgly 120
Db 301 GATTACACCTTATCCACGTTACGAAACCAACCTGTAACACATTCAGGGGTTTGACAGCT 360
Qy 121 LeuThrThrSerLeuSerThrLeuAsnAlaProAlaLeuSerArgThrgIlnSerAspGly 140
Db 361 TTAACCACTTTCTTTATCTTACACTTAATATCCCTGCACTCTCTCGAACCAATACAGCT 420
Qy 141 SerGlySerArgSerSerLeuGlyLeuAsnIleGlyGlyMetGlyAspTYrArgAsnGlu 160
Db 421 AGCGGAAGTAAAGACAGTCTGGGCTTAATATTTGGCGGAGTGGGGATTATGAAATGAA 480
Qy 161 ThrLeuThrThraenProArgAspThralaPheLeuSerHisLeuValGlnThralaPhe 180
Db 481 ACCTTGAGACTTAACCCCGCGGACACTGCTTTCTTCCACTTGTAACAGCCGCTATT 540
Qy 181 PheLeuArgGlyIleAspValIleSerProAlaAsnAlaAspThrAspValPheIleAsn 200
Db 541 TTCCTGGCGGCAATAGAGCTTTCTCTCTGCCAATGCCGATACAGATGTTATTAAAC 600
Qy 201 IleAspValPheGlyThrIleArgAsnArgThrgIuMetHisLeuTYrAsnAlaGluThr 220
Db 601 ATCGACGTAATCGGAACGATACGAAACAGAACCGAAATGACCTTATACAAATCCGAAACA 660
Qy 221 LeuIyAsnIleGlnThrlyLeuGluTYrPheAlaValaAspArgThralaLeuIleLeu 240
Db 661 CTGAAGCCCAACCAACCTGAAATATTTCCAGATGACAGAACCAATATAAATTGCTC 720
Qy 241 IleyPProLySThrAsnAlaPheGluAlaAlaIYrlyGluAsnTYrAlaLeuTrpMet 260
Db 721 ATCAACCAAAACCAATGCGTTGAGCTGCTTAAAGAAATTACGCAATTGGATG 780
Qy 261 GYProTYrlyValSerlyGlyIYrlySerProThrgluGluLeuMetValAspPheSer 280
Db 781 GGGCGGTATAAGTAAGCAAGAAATTAACCGACGAAAGATTAATGTCGATTTCTCC 840

Qy 281 AsplleArProYrGlyAsnHieThrGlyAsnSerAlaProSeValGluaLaAspAsn 300
Db 841 GATATCCGACCATACGGCAATCATACGGGTAACTCCGCCCATCCGTAGAGGCTGATAC 900
Qy 301 SerHisGluGlyTYrGlyTYrSerAspGluAlaValArgGlnHisArgGlnGlyGlnPro 320
Db 901 AGTCATGAGGGGTATGATACAGCGATGAAGTAGTCAGACAACATAGACAAGGACAACT 960
RESULT 10
AA254613 standard; DNA; 963 BP.
XX AA254613;
AC AA254613;
XX
DT 21-MAR-2000 (first entry)
XX
DE Neisseria meningitidis ORF 406 partial DNA sequence SEQ ID NO:3109.
XX
KM Neisseria meningitidis; Neisseria gonorrhoeae; antigen; vaccine;
KM antigenic; diagnosis; immunogenic; infection; meningitis; septicaemia;
KM antibacterial; gene therapy; ds.
XX
OS Neisseria meningitidis.
XX
PN WO957280-A2.
XX
PD 11-NOV-1999.
XX
PF 30-APR-1999; 99WO-US009346.
XX
XX 01-MAY-1998; 98US-0083758P.
PR 31-JUL-1998; 98US-0094869P.
PR 02-SEP-1998; 98US-0098994P.
PR 02-SEP-1998; 98US-0099062P.
PR 09-OCT-1998; 98US-0103749P.
PR 09-OCT-1998; 98US-0103794P.
PR 09-OCT-1998; 98US-0103796P.
PR 25-FEB-1999; 99US-0121528P.
XX
PA (CHIR) CHIRON CORP.
PA (GENO-) INST GENOMIC RES.
XX
XX Fraser C, Galeotti C, Grandi G, Hickey E, Masignani V, Mora M;
PI Petersen J, Pizzo M, Rappuoli R, Ratti G, Scalati E, Scarselli M;
PI Tettelin H, Venter JC;
XX
DR WPI; 2000-062150/05.
DR P-PSDB; AAY75811.
XX
PT Novel Neisserial polypeptides predicted to be useful antigens for
XX vaccines and diagnostics.
PS
PS Example 1; Page 108-109; 1453pp; English.
XX
XX AA253015 to AA254536, AA254577 to AA254615, and AAY74253 to AAY75941
CC represent novel Neisseria meningitis and N. gonorrhoeae polynucleotides
CC and polypeptides. AA254537 to AA254576 and AA254616 to AA254617 represent
CC PCR primers used in the exemplification of the present invention. The
CC polypeptides, the polynucleotides, antibodies and compositions of the
CC invention can be used as vaccines, as diagnostic reagents, and as
CC immunogenic compositions. The polypeptides can be used in the manufacture
CC of medicaments for treating or preventing infection due to Neisserial
CC bacteria (e.g. meningitis and septicaemia), to detect the presence of
CC Neisseria bacteria, or to raise antibodies. They may also be used to
CC screen for agonists or antagonists, which may themselves have used as
CC antibacterial agents. The polynucleotides of the invention may also be
CC used in gene therapy protocols
XX
SQ Sequence 963 BP; 284 A; 234 C; 217 G; 228 T; 0 U; 0 Other;
Alignment Scores: 1,34e-157 Length: 963
Pred. No.: 1634.00 Matches: 317
Score:

Percent Similarity: 99.69% Conservative: 2
Best Local Similarity: 99.06% Mismatches: 1
Query Match: 99.33% Indels: 0
DB: 3 Gaps: 0
US-10-617-835-4 (1-320) x AA254613 (1-963)
Qy 1 MetArgAlaArgLeuLeuLeuProIleuPheSerValPheIleLeuSerAlaCysGly 20
Db 1 ATGCAGACGAGCGCTGCTGATACCTTATCTTTTCAGTTTATTTATTCGCGCTCGCGG 60
Qy 21 ThrLeuThrGlyIleProSerHisGlyGlyGlyLysArgPheAlaValGlnGlnLeu 40
Db 61 ACACGTGACAGGTATTCATCGCATGCGGAGGTAAACGCTTGGCGTGAAACAAGACTT 120
Qy 41 ValAlaAlaSerAlaArgAlaAlaValLysAspMetAspLeuGlnAlaLeuHisGlyArg 60
Db 121 GTGGCCGCTCTGCGCAAGCTGCGCTTAAAGACATGATTTACAGGCACTTACAGGACGA 180
Qy 61 LysValAlaLeuTYrIleAlaThrMetGlyAspGlnGlySerGlySerLeuThrGlyGly 80
Db 181 AAAGTTGCATTGTATTCATTGCCACATAGGGCGACCAAGGTTCAAGGCAAGGGGGGT 240
Qy 81 ArgTYrSerIleAspAlaLeuIleArgGlyGlyTYrIleAsnSerProAlaValArgThr 100
Db 241 CGTACTCTCATTTGATGACGATGATTCGTGCGAATACATAAACAGCCCTGCGCTCGTACC 300
Qy 101 AspTYrThrTYrProArgTYrGluThrThrAlaGlnThrThrSerGlyGlyLeuThrGly 120
Db 301 GATTACACCTTATCCACGTTACGAAACACCGCTAAACACATACAGGCGGTTTACAGGT 360
Qy 121 LeuThrThrSerLeuSerThrLeuAsnAlaProAlaLeuSerArgThrGlnSerAspGly 140
Db 361 TTACACACTTCTTATATCATCACTTAATGCCCCCTGCACCTCTCCACCAATCAGACGGT 420
Qy 141 SerGlySerArgSerSerLeuGlyLeuAsnIleGlyGlyMetGlyAspTYrArgAsnGlu 160
Db 421 AGCGAAGTAAACACAGCTGGGCTTAAATATTTGCGGGAAGGGGGAATTACGAAAGTAA 480
Qy 161 ThrLeuThrThrAsnProArgAspThrAlaPheLeuSerHisLeuValGlnThrValPhe 180
Db 481 ACCTTGACGACTTACCCGCGGACACACTGCTTTTCCCTGCGTACAGACCGTATTT 540
Qy 181 PheLeuArgGlyIleAspValValSerProAlaAsnAlaAspThrAspValPheIleAsn 200
Db 541 TTCCTGGCGGCAATAGAGCTTTCTTCCTGCAATGCCATACAGATGTGTTATTATAC 600
Qy 201 IleAspValPheGlyThrIleArgAsnArgThrGluMetHisLeuTYrAsnAlaGluThr 220
Db 601 ATCGACGTATTCGGAACGATACGCAACGAACCCGAATGCCTTATCAATGCCGAACA 660
Qy 221 LeuLysAlaGlnThrLysLeuGluTYrPheAlaValAspArgThrAsnLysLeuLeu 240
Db 661 CTGAAGCCCAAAACAAACCTGAAATATTTGCGATACAGAACCAATAAAATTTGCTC 720
Qy 241 IleLysProIleThrAsnAlaPheGluAlaAlaTYrLysGluAsnTYrAlaLeuTYrMet 260
Db 721 ATCAAAACCAAAAACCAATAGCTTTGAAGCTGCCCTTAAAGAAATTTGCGCTTGTGATG 780
Qy 261 GlyProTYrLysValSerLysGlyIleLysProThrGlnGlyLeuMetValAspPheSer 280
Db 781 GGGCGGATTAAGTAACCAAAAGGAATTAACCGAGGAGGATTAATGATTTCTCC 840
Qy 281 AsplleArProYrGlyAsnHieThrGlyAsnSerAlaProSeValGluaLaAspAsn 300
Db 841 GATATCCGACCATACGGCAATCATACGGGTAACTCCGCCCATCCGTAGAGGCTGATAC 900
Qy 301 SerHisGluGlyTYrGlyTYrSerAspGluAlaValArgGlnHisArgGlnGlyGlnPro 320
Db 901 AGTCATGAGGGGTATGATACAGCGATGAAGTAGTCAGACAACATAGACAAGGACAACT 960
RESULT 11
AAA81296

ID AAA01296 standard; DNA; 963 BP.
 XX AAA01296;
 AC
 XX 04-DEC-2000 (first entry)
 DT
 XX
 XX N. meningitidis partial DNA sequence m406.seq seq ID NO:1034.
 DE
 XX Neisseria meningitidis; Neisseria gonorrhoeae; genome; immunogenic;
 KM antigen; vaccine; diagnosis; infection; antibacterial; identification;
 KW Meningococcus B; Mening. ds.
 XX
 XX Neisseria meningitidis.
 OS
 XX WO200022430-A2.
 PN
 XX 20-APR-2000.
 PD
 XX 08-OCT-1999; 99WO-US023573.
 PF
 XX 09-OCT-1998; 98US-0103794P.
 PR 30-APR-1999; 99US-0132068P.
 XX
 XX (CHIR) CHIRON CORP.
 PA
 PI Frazer CM, Hickey E, Peterson J, Tettelin H, Venter JC, Scarlato V,
 PI Maignani V, Galeotti C, Mora M, Ratti G, Scarselli M, Scarlato V,
 PI Rapuoli R, Pizzi M;
 DR WPI; 2000-318079/27.
 XX P-PsDB; AAB25656.
 DR
 XX
 PT Isolated nucleotide sequences of Neisseria meningitidis which can be used
 PT in the diagnosis and treatment of N. meningitidis infection and other
 PT Neisserial infections, for example, N.gonorrhoea.
 PS
 XX Class 9; Page 107; 1760pp; English.
 XX
 CC The present invention describes methods of obtaining immunogenic proteins
 CC from Neisseria genomic sequences. AAA01453 to AAA02414 represent
 CC specifically claimed Neisseria meningitidis genomic DNA sequences;
 CC AAA01260 to AAA01303 and AAB25620 to AAB25663 represent Neisseria DNA
 CC sequences and their corresponding proteins; AAA01254 to AAA01259 and
 CC AAA01304 to AAA01321 represent PCR primers used in the isolation of
 CC Neisseria meningitidis DNA sequences; and AAA01322 to AAA01452 represent
 CC Neisseria meningitidis MenB polynucleotide ORF sequences, which are all
 CC used in the exemplification of the present invention. The nucleic acid
 CC sequences, protein sequences, and antibodies against them, can be used in
 CC the manufacture of a composition. The composition can be used as a
 CC medicament (or in the manufacture of a medicament) for treating,
 CC preventing or diagnosing infection due to Neisserial bacteria. For
 CC example, some of the identified proteins could be components of vaccines
 CC against Meningococcus B; against all serotypes; and/or against all
 CC pathogenic Neisseriae. Identification of sequences from the bacterium
 CC will also facilitate production of biological probes, particularly
 CC organism-specific probes. Attempts to make efficacious Meningococcus B
 CC vaccines have failed mainly due to antigen tolerance. Multivalent
 CC antigens have also been tried but none have successfully overcome
 CC antigenic variability. The provision of further, complete sequences may
 CC provide an opportunity to identify secreted or surface exposed proteins
 CC that may be presumed targets for the immune system and which are not
 CC antigenically variable or at least more conserved than other more
 CC variable regions
 XX
 XX Sequence 963 BP; 284 A; 234 C; 217 G; 228 T; 0 U; 0 Other;
 SQ
 Alignment Scores:
 Pred. No.: 1,34e-157 Length: 963
 Score: 1634.00 Matches: 317
 Percent Similarity: 99.69% Conservative: 2
 Best Local Similarity: 99.06% Mismatch: 1
 Query Match: 99.33% Indels: 0
 DB: 3 Gaps: 0

US-10-617-835-4 (1-320) x AAA01296 (1-963)
 QY 1 MetArgAlaArgLeuLeuLeuProIleuPheSerValPheIleuSerAlaCysGly 20
 DB 1 ATGCAAGCAGCGCTGCTGATACCTATTCTTTTTCAGTTTATTATTATCCGCTCGGG 60
 QY 21 ThrLeuThrGlyIleProSerHisGlyGlyValArgPheAlaValGluGluGlu 40
 DB 61 ACACGACACGATTCATTCATGATGCGGAGGATTAACGCTTTGCGGTCAACAAGAACTT 120
 QY 41 ValAlaAlaSerAlaArgAlaAlaValLysAspMetAspLeuGlnAlaLeuHisGlyArg 60
 DB 121 GTGGCCGCTTCTCCAGAGCTCCGTTAAAGACATGATTTACAGGATTAACAGCA 180
 QY 61 LysValAlaLeuTyrlleAlaThrMetGlyAspGlnGlySerGlySerLeuThrGlyGly 80
 DB 181 AAAGTTGCATGTTGATCATTTGCCACTATGGGCGACCAAGGTTCAAGGAGTTGACAGGGGGT 240
 QY 81 ArgTyrSerIleAspAlaLeuIleArgGlyGlyIleLysSerProAlaValArgThr 100
 DB 241 CGCTACCTCATTTGATGACACTGATTCGTGGCGAATACATTAACAGCCCTCCGCTAC 300
 QY 101 AspTyrThrTyrProArgTyrGluThrThrAlaGluThrThrSerGlyGlyLeuThrGly 120
 DB 301 GATTACACCTATCCACGTTACGAAACACCGCTGAACAACATCAAGCGGTTGACAGGT 360
 QY 121 LeuThrThrSerLeuSerThrLeuAlaAlaProAlaLeuSerArgThrGlnSerAspGly 140
 DB 361 TTAAACCACTTCTTATCTACACTTAATGCCCCCTGCACCTCTCGCACCAATCAGACGGT 420
 QY 141 SerGlySerArgSerSerLeuGlyLeuMetIleGlyGlyMetGlyAspTyrArgGlu 160
 DB 421 ACCGGAAGTAAAGAGATCTGGCTTAATATTTGGCGGATGAGGATTAATGAATGA 480
 QY 161 ThrLeuThrThrAspProArgAspThrAlaPheLeuSerHisLeuValGlnThrValPhe 180
 DB 481 ACCTTGACACCTAACCCGCGGACACTGCTTCTTCCCACTGTTGACAGCCGATTT 540
 QY 181 PheLeuArgGlyIleAspValSerProAlaAlaAspThrAspValPheIleAla 200
 DB 541 TTCCTGCGGCGATAGACGTTGTTCTCTCGCAATGCGGATACAGATGTGTTATTAC 600
 QY 201 IleAspValPheGlyThrIleArgAsnArgThrGluMetHisLeuTyrAsnAlaGluThr 220
 DB 601 ATCGACGTAATTCGAAACGATAGCAACAGAACCGAAATGCACCTATACAAATCCGAAACA 660
 QY 221 LeuLysAlaGlnThrLysLeuGluTyrPheAlaValAspArgThrAsnLysLysLeu 240
 DB 661 CTGAAGCCCAACAACTGGAATTTTCGAGTACAGAACCAATTAATAATGCTC 720
 QY 241 IleLysProLysThrAsnAlaPheGluAlaAlaTyrLysGluAsnTyrAlaLeuTyrMet 260
 DB 721 ATCAAAACCAAAACCAATGCGTTGAGTCGCTTAAAGAAATATACCATTTGCGAAG 780
 QY 261 GlyProTyrLysValSerLysGlyIleLysProThrGluGlyLeuMetValAspPheSer 280
 DB 781 GGGCGGTAAAGTAAGCAAGAAATTAACCGACGAAAGATTAATGATTCATTTCTC 840
 QY 281 AspIleAspProTyrGlyAsnHisThrGlyAsnSerAlaProSerValGluAlaAspAsn 300
 DB 841 GATATCCGACCATAGCGGCAATATACGGTAACTCCGCCCATCCGTAGAGGCTGATAC 900
 QY 301 SerHisGluGlyTyrGlyTyrIserAspGluAlaValArgGlnHisArgGlnGlyPro 320
 DB 901 AGTCATGAGGGGTATGATATACAGCATGAAATGAGCGCAACATATGACAAAGACAACT 960
 RESULT 12
 AAF21581
 ID AAF21581 standard; DNA; 963 BP.
 XX
 AC AAF21581;
 XX

DT 13-MAR-2001 (first entry)
DE N. meningitidis partial DNA sequence m406.seq SEQ ID NO: 74.
XX
XX
XX Neisseria meningitidis; Neisseria gonorrhoeae; immunogenic; vaccine;
KW diagnosis; antigen; detection; infection; gene therapy; antibacterial;
XX ds.
XX
OS Neisseria meningitidis.
XX
XX
XX WO20006791-A1.
XX
XX
XX 09-NOV-2000.
XX
XX
XX 08-MAR-2000; 2000MO-US005928.
XX
XX
XX 30-APR-1999; 99US-0132068P.
XX 08-OCT-1999; 99WO-US021573.
XX 28-FEB-2000; 2000GB-00004695.
XX
XX
XX (CHIR) CHIRON CORP.
XX (GENO-) INST GENOMIC RES.
XX
XX
XX Pizza M, Hickey B, Peterson J, Tettelin H, Venter JC;
XX Masignani V, Galeotti C, Mora M, Ratti G, Scarsella M, Scarlato V;
XX Rappuoli R, Frazer CM, Grandi G;
XX
XX WPI: 2000-647603/62.
XX P-PSDB: AAB58586.
XX
XX
XX Neisseria meningitidis B full length genome sequence and open reading
XX frames are used to detect, treat and prevent Neisserial infections.
XX
XX
XX Example 1; Page 108; 692pp; English.
XX
XX
XX The present invention describes the full length genome of Neisseria
XX meningitidis B (NMB). The sequences in AAF21544 and AAF21607 to AAF21613
XX represent fragments of the NMB genomic sequence, as the sequence was too
XX long to go in a record on its own. It was split into 8 sequences which
XX overlap each other at the beginning and end of each sequence by 49980 bp
XX (i.e. the last 49980 bp of AAF21544 is repeated at the beginning of
XX AAF21607, the last 49980 bp of AAF21607 are repeated at the beginning of
XX AAF21608, and so on). AAF21545 to AAF21588 encode the Neisseria proteins
XX given in AAB58550 to AAB58593, and AAF21589 to AAF21606 represent PCR
XX primers which are used in the exemplification of the present invention.
XX The NMB genome and fragments from it have antibacterial activity, and can
XX be used in vaccines and gene therapy. Neisseria nucleic acids, proteins
XX and/or antibodies which binds to the proteins can be used in compositions
XX for treating or preventing infection due to Neisserial bacteria or as a
XX diagnostic reagent for detecting the presence of Neisserial bacteria or
XX of antibodies raised to Neisserial bacteria. Computers, computer memory,
XX computer storage medium or computer databases can be used in a search to
XX identify open reading frames (ORFs) or coding sequences within the NMB
XX genome. The DNA sequences provide further opportunities to find antigenic
XX or immunogenic proteins which are more effective in vaccines than the
XX outer membrane proteins currently used

SO Sequence 963 BP; 284 A; 234 C; 217 G; 228 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	1.34e-157	Length:	963
Score:	1634.00	Matches:	317
Percent Similarity:	99.69%	Conservative:	2
Best Local Similarity:	99.06%	Mismatches:	1
Query Match:	99.33%	Indels:	0
DB:	3	Gaps:	0

US-10-617-835-4 (1-320) x AAF21581 (1-963)

QY 1 MetARGAAlaArgLeuIleuLeuProIleLeuPheSerValPheIleuSerAlaCysGly 20
1 ATGCAAGACGCGCTCTGTACTACTATCTTTTTCAGTTTATTTTATTCGCGCTCGCG 60

QY	21	ThrLeuThnGlyIleProSerHisgIyGlyIyLysArgPheAlaValGluGlnGluLeu	40
Db	61	ACACTGACAGGATTTCATCGCATGCGAGGTAACCGCTTTCGGCTCGACAAAGAACTT	120
QY	41	ValAlaAlaSerAlaArgAlaAlaValLysAspMetAspLeuGlnAlaLeuHisgIyArg	60
Db	121	GTGGCCGGCTTCTGGCCAGAGCTCCCGTTAAAGACATGATTTTCAGGCATTTACACGACGA	180
QY	61	LysValAlaIaLeuTyrTlleAlaThrMetGlyAspGlnGlySerGlySerLeuThnArgIyGly	80
Db	181	AAAGTTGACATGTGTACATTGCCCTATGGCGGACCAAGTTCCAGGCGTTTGACAGGGGGT	240
QY	81	ArgTyrSerIleAspAlaLeuIleArgGlyGluTyrTlleAsnSerProAlaValArgThr	100
Db	241	CGCTACTCCATTGATGACGACTGATTCGTGGCGAATACATAAACAGCCCTCCGCTCGTAC	300
QY	101	AspTyrThrTyrProArgTyrGluThrThrAlaGluThrThrSerGlyGlyLeuThnGly	120
Db	301	GATTACACCTATCCAGCGTTACCAAAACACCGCTGAAACAACTACAGCGGTTTGACAGGT	360
QY	121	LeuThnThrSerLeuSerThrLeuAsnAlaProAlaLeuSerArgThrGlnSerAspGly	140
Db	361	TTAACCACTCTTTATCTACACTTAATGCCCTCGACTCTTCGCAACCAATACAGCGGT	420
QY	141	SerGlySerArgSerSerLeuGlyLeuAsnIleGlyGlyMetGlyAspTyrArgAsnGlu	160
Db	421	AGCGAGAGTAAAGACAGCTGGGCTTAAATTTGGCGGGATGGGGGATTATCGAAATGAA	480
QY	161	ThrLeuThrThrAsnProArgAspThrAlaPheLeuSerHisLeuValGlnThrValPhe	180
Db	481	ACCTTGACAGCACTAACCCGCGCACACTGCTTTCTTCCACTTGGTACAGACCGTAATT	540
QY	181	PheLeuArgGlyIleAspValValSerProAlaAsnAlaAspThrAspValPheIleAsn	200
Db	541	TTCCGCGCGCGATAGAGCTGTGTTCTCCTGGCAATGCCGATACAGATGTGTTATTAAAC	600
QY	201	IleAspValPheGlyThrTlleArgAsnArgThrGluMetHisLeuTyrAsnAlaGluThr	220
Db	601	ATCGACGATTATCGGAACATACGCAACAGAACCGAAATGCACCTAATCAATGCGCAACCA	660
QY	221	LeuLysAlaGlnThrLysLeuGluTyrPheAlaValaAspArgThrAsnLysLysLeuLeu	240
Db	661	CTGAAGGCCCAACCAAACTGGAATATTTCCGAGTATGACAGAACCAATAAAAAAATTGCTC	720
QY	241	IleLysProLysThrAsnAlaPheGluAlaAlaTyrLysGluAsnTyrAlaLeuTyrMet	260
Db	721	ATCAAAACCAAAAAACAATGCCGTTTGAAAGCTGCTTAAAGAAATTAATCCCATTTGTCGATG	780
QY	261	GlyProTyrLysValSerLysGlyIleLysProTnGlnGlyLeuMetValAspPheSer	280
Db	781	GGGCGGTAAAGTAAGCAAGAAAGATTAAACGACGAAAGGATTATTTGGTTCGATTTCTCC	840
QY	281	AspIleArgProTyrGlyAsnHisThrGlyAsnSerAlaProSerValGluAlaAspAsn	300
Db	841	GATATCCGACCATACGAGCATCATACGGGTACTCCGCCCATCCGTAGAGGCTGATTAAC	900
QY	301	SerHisGluGlyTyrGlyTyrSerAspGluAlaValaArgGlnHisArgGlnGlyGlnPro	320
Db	901	AGTCATGAGGGGTATGATACAGCATGAAGTAGTGCACCAATATGACAAAGACAACCT	960
RESULT 13			
AAZ13007			
ID AAZ13007 standard; DNA, 963 BP.			
XX	AAZ13007;		
AC	08-OCT-1999 (first entry)		
XX			
XX	Neisseria meningitidis strain A complete ORF15 sequence.		
DE			
XX	Neisseria meningitidis, Neisseria gonorrhoeae, antigen; vaccine;		
KW	treatment; Neisseria infection; meningitis; septicemia; gonorrhea; ss.		
XX			

OS Neisseria meningitidis.
 XX
 PN W09924578-A2.
 XX
 PD 20-MAY-1999.
 XX
 PF 09-OCT-1998; 98WO-1B001665.
 XX
 PR 06-NOV-1997; 97GB-00023516.
 PR 14-NOV-1997; 97GB-00024190.
 PR 18-NOV-1997; 97GB-00024386.
 PR 27-NOV-1997; 97GB-00025158.
 PR 10-DEC-1997; 97GB-00026147.
 PR 14-JAN-1998; 98GB-00000759.
 PR 01-SEP-1998; 98GB-00019016.
 XX
 PA (CHIR-) CHIRON SPA.
 XX
 PI Masignani V, Rappunoli R, Pizza M, Scarlato V, Grandi G;
 DR WPI; 1999-327407/27.
 DR P-PSDB; AAY38539.
 XX
 PT Proteins from Neisseria meningitidis and N. gonorrhoeae useful for
 XX diagnosis, treatment and prevention of infection.
 XX
 PS Claim 9; Page 98; 524pp; English.
 XX
 CC Nucleotide sequences AA211972-212358 represent open reading frames (ORFs)
 CC of Neisseria meningitidis and N. gonorrhoeae which encode antigenic
 CC proteins (see AAY38499-Y38944). The antigenic proteins, their fragments,
 CC their nucleic acids and antibodies are used for diagnosis, prevention (as
 CC vaccines) or treatment of Neisseria infections, such as meningitis,
 CC septicemia and gonorrhea. Both organisms are closely related. Fragments
 CC of the nucleic acids are useful as hybridisation probes and antisense
 CC reagents
 XX
 SQ Sequence 963 BP; 285 A; 232 C; 218 G; 228 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 1,42e-156 Length: 963
 Score: 1624.00 Matches: 315
 Percent Similarity: 99.69% Conservative: 4
 Best Local Similarity: 98.44% Mismatches: 1
 Query Match: 98.72% Indels: 0
 DB: 2 Gaps: 0
 US-10-617-835-4 (1-320) x AA212007 (1-963)
 QY 1 MetATGATGAATGLeuLeuLeuLeuLeuLeuPheIleuSerValPheIleuSerAlaCysGly 20
 DB 1 ATGCAAGACGGCTCTGATACCTATCTTTTATGATTTTATTTATCCCGCTGCGGG 60
 QY 21 ThrLeuThrGlyIleProSerHisGlyGlyGlyLeuPheAlaValGluGlnGluLeu 40
 DB 61 ACACCTGACAGGATTCATCCATCGATGCGGAGGTAAACGCTTTCGCGTGAACAAGACTT 120
 QY 41 ValAlaAlaSerAlaIleAlaAlaValIleAspMetAspLeuGlnAlaLeuHisGlyArg 60
 DB 121 GTGGCGGCTTCTGCAGAGCTGCCGTTAAAGACATGATTTTACAGGCATTAACAGGAGA 180
 QY 61 LysValAlaLeuTyrIleAlaThrMetGlyAspGlnGlySerGlySerLeuThrIleGly 80
 DB 181 AAAGTTGCACTGTATGCAATGCAATGCGGACCAAGGTTTCAGGAGTTGACAGGGGGT 240
 QY 81 ArgTyrSerIleAspAlaLeuIleArgGlyGlyTyrIleAsnSerProAlaValArgThr 100
 DB 241 CGCTACTCATTTGATGCACTGATTCGTGCGAATACATAAAGCCCTGCGCTCGTAC 300
 QY 101 AspTyrThrTyrProArgTyrGluThrThrAlaGluThrThrSerGlyLeuThrGly 120
 DB 301 GATTACACCTATCCAGTTACGAAACCAACCCCTGAAACAAATCATCAGGCGGTTTGACAGGT 360

QY 121 LeuThrThrSerLeuSerThrIleuAsnAlaProAlaLeuSerArgThrGlnSerAspGly 140
 DB 361 TTACACACTCTTTATATTAACCTTAATAGCCCTTGACCTCTCGGACCAATCAGACGGT 420
 QY 141 SerGlySerArgSerSerLeuGlyLeuAsnIleGlyGlyMetGlyAspTyrArgAsnGly 160
 DB 421 AGCGAAGATGAAGACAGTCTGGGCTTAAATATATGCGGGATGGGGGATTAATGAATGA 480
 QY 161 ThrLeuThrThrAsnProArgAspThrAlaPheLeuSerHisLeuValGlnThrValPhe 180
 DB 481 ACCTTGACGACTTAACCCGCGACACTGCTCTTTCTCCACTTGATGACAGCCGATTT 540
 QY 181 PheLeuArgGlyIleAspValValSerProAlaAsnAlaAspThrAspValPheIleAsn 200
 DB 541 TTCCTGCGGCGATAGAGGTGTTTCTCTGCAATGCGATACGATATGTTTATTAAAC 600
 QY 201 IleAspValPheGlyThrIleArgAsnArgThrGluMetHisLeuTyrAsnAlaGluThr 220
 DB 601 ATCGACGTTTTCGGAACGATACGCAACGAAACCGAAATGCACCTTATCAATCCGAAACA 660
 QY 221 LeuLysAlaGlnThrLysLeuGluTyrPheAlaValAspArgThrAsnLysLeuLeu 240
 DB 661 CTGAAGCCCAAAACAACTGGATATTTCCGATGACAGAACCAATTAATAAATTGCTC 720
 QY 241 IleLysProLysThrAsnAlaPheGluAlaIleTyrLysGluAsnTyrAlaLeuThrPhe 260
 DB 721 ATCAAAACCAAAACCAATGCTTGAACCTGCTTAAAGAAATTAACCATTTGGATG 780
 QY 261 GlyProTyrLysValSerLysGlyIleLysProThrGluGlyLeuMetValAspPheSer 280
 DB 781 GGACCGTTAAAGTAAGCAAGGATTAACCGACAGAAAGATTATGTCGATTTCTC 840
 QY 281 AspIleArgProTyrGlyAsnHisThrGlyAsnSerAlaProSerValGluAlaAspAsn 300
 DB 841 GATTATCCAAACCATAGGCAATCATATGATGATCTGCCCCATCCGTAGAGGCTCATAAC 900
 QY 301 SerHisGluGlyTyrGlyTyrSerAspGluAlaValArgGlnHisArgGlnGlyInPro 320
 DB 901 AGTCATGAGGGGTATGATATACGATGACGATGACGATGACGACATGACAAAGGCACT 960
 RESULT 14
 AA254615
 ID AA254615 standard; DNA; 963 BP.
 AC AA254615;
 XX
 DT 21-MAR-2000 (first entry)
 XX
 DE Neisseria meningitidis ORF 406 partial DNA sequence SEQ ID NO:3113.
 XX
 KW Neisseria meningitidis; Neisseria gonorrhoeae; antigen; vaccine;
 KW antigenic; diagnosis; immunogenic; infection; meningitis; septicemia;
 KW antibacterial; gene therapy; ds.
 OS Neisseria meningitidis.
 XX
 PN W09957280-A2.
 PD 11-NOV-1999.
 XX
 PF 30-APR-1999; 99WO-US009346.
 XX
 PR 01-MAY-1998; 98US-0083758P.
 PR 31-JUL-1998; 98US-0094869P.
 PR 02-SEP-1998; 98US-0098994P.
 PR 02-SEP-1998; 98US-0099062P.
 PR 09-OCT-1998; 98US-0103749P.
 PR 09-OCT-1998; 98US-0103794P.
 PR 09-OCT-1998; 98US-0103796P.
 PR 25-FEB-1999; 99US-0121528P.
 XX
 PA (CHIR-) CHIRON CORP.
 PA (GENO-) INST GENOMIC RES.

XX Fraser C, Galeotti C, Grandi G, Hickey E, Masignani V, Mora M;
PI Petersen J, Pizzo M, Rappuoli R, Ratti G, Scalato E, Scarselli M;
PI Tettelin H, Venter JC;
XX
DR WPI: 2000-062150/05.
XX P-PSDB; AAY75813.
XX
PT Novel Neisserial polypeptides predicted to be useful antigens for
PT vaccines and diagnostics.
XX
PS Example 1, Page 110; 1453bp; English.
XX
CC AA253015 to AA254536, AA254577 to AA254615, and AAY74253 to AAY75941
CC represent novel *Neisseria meningitidis* and *N. gonorrhoeae* polynucleotides
CC and polypeptides. AA254537 to AA254576 and AA254616 to AA255473 represent
CC PCR primers used in the exemplification of the present invention. The
CC polypeptides, the polynucleotides, antibodies and compositions of the
CC invention can be used as vaccines, as diagnostic reagents, and as
CC immunogenic compositions. The polypeptides can be used in the manufacture
CC of medicaments for treating or preventing infection due to *Neisseria*
CC bacteria (e.g. meningitis and septicemia), to detect the presence of
CC *Neisseria* bacteria, or to raise antibodies. They may also be used to
CC screen for agonists or antagonists, which may themselves have use as
CC antibacterial agents. The polynucleotides of the invention may also be
CC used in gene therapy protocols
XX
SQ Sequence 963 BP; 285 A; 233 C; 218 G; 227 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 1,42e-156 Length: 963
Score: 1624.00 Matches: 315
Percent Similarity: 99.69% Conservative: 4
Best Local Similarity: 98.44% Mismatches: 1
Query Match: 98.72% Indels: 0
DB: Gaps: 0

US-10-617-835-4 (1-320) x AA254615 (1-963)

QY 1 MetArgAlaArgLeuLeuIleProIleLeuPheSerValPheIleLeuSerAlaCysGly 20
Db 1 ATGGAGACGCGCGTGTGATACCTATTCTTTTTCAGTTTATTATTATTCGCGCTGCGG 60
QY 21 ThrLeuThrglyIleProSerHisGlyGlyGlyValSerArgPheAlaValGlnGlnIleu 40
Db 61 ACACGTGACAGGATATTCATCGCATGCGGAGGTAAACCTTCGCGGTGAGAACAGACTT 120
QY 41 ValAlaAlaSerAlaArgAlaAlaValIleAspMetAspLeuGlnAlaLeuHisGlyArg 60
Db 121 GTGGCCGCTTCTGCCAGAGCTGCCGTTAAAGACATGATTAAACAGGCACTTACAGGACGA 180
QY 61 LysValAlaLeuValIleAlaThrMetClyAspGlnGlySerGlySerLeuThrgly 80
Db 181 AAAGTTGATGATTCATTGCAACTATGAGCGACCAAGGTTGACGAGATTGACAGGGGCT 240
QY 81 ArgTyrSerIleAspAlaLeuIleArgGlyGlyIleuValSerProAlaValArgThr 100
Db 241 CGCTACTCCATTGATGCACTGATTCGTGGCAATACATAAACAGCCCTGCGTCCGTACC 300
QY 101 AspTyrThrTyrProArgTyrGlyThrThrAlaGluThrThrSerGlyGlyLeuThrgly 120
Db 301 GATTACACCTATCCACGTTACGAAACACACCCGCTGAACAAACATGAGCGGCTTTCACAGGT 360
QY 121 LeuThrThrSerLeuSerThrLeuAsnAlaProAlaLeuSerArgThrGlnSerAspGly 140
Db 361 TTAAACCACTTCTTATCTACACTTAATGCCCTCGACTCTGCGCACCAATTCAGACGCT 420
QY 141 SerGlySerArgSerSerLeuGlyLeuAsnIleGlyGlyMetGlyAspTyrArgAsnGlu 160
Db 421 AGCGGAAGTAAACACAGCTGCGCTTAAATTTGGCGGAGATGGGGGATTATCGAAATCAA 480
QY 161 ThrLeuThrThrAsnProArgAspThrAlaPheLeuSerHisLeuValGlnThrValPhe 180

Db 481 ACCTTAGACACTAACCCGCGGACACTGCTTCTTCCCACTTGATACACCGTATTT 540
QY 181 PheLeuArgGlyIleAspValValSerProAlaAsnAlaAspThrArgValPheIleAsn 200
Db 541 TTCTGCGCGGACATAGACGTTGTTCTTCCTGCCAATGCCATGAGATGTTATTATTAAC 600
QY 201 IleAspValPheGlyThrIleArgAsnArgThrGlnMetHisLeuTyrAsnAlaGluThr 220
Db 601 ATCGACGATTTCCGAAACGATACGCAACGAAACGAAATGCACCTTACAAATGCCGAAACA 660
QY 221 LeuLysAlaGlnThrIleLysLeuGlyThrPheAlaValAspArgThrAsnLysLeuLeu 240
Db 661 CTGAAGCCCAAACAAACAACTGCAATATTTCGCACTATACAGAACCAATTAATAATGCTC 720
QY 241 IleLysProLysThrAsnAlaPheGluAlaAlaTyrLysGluAsnTyrAlaLeuThrMet 260
Db 721 ATCAACCAAAACCAATGCGTTTGAAGCTGCTTAAAGAAATTAACGCAATGTGGATG 780
QY 261 GlyProTyrLysValSerLysGlyIleLysProThrGlnGlyLeuMetValAspPheSer 280
Db 781 GGACCGTNTAAAGTAAACCAAGAAATTAACCGACAGAGATTAAATGTCGATTTCTCC 840
QY 281 AspIleArgProTyrGlyAsnHisThrGlyAsnSerAlaProSerValGluAlaAspAsn 300
Db 841 GATATCCACCATACGCGCAATCATATGCTAACTCTGCCATCTCGTAGAGGCTGATTAAC 900
QY 301 SerHisGlnGlyTyrGlyTyrSerAspGluAlaValArgGlnHisArgGlnGluPro 320
Db 901 AGTCATAGAGGATGATGATTAACGCAATGAAGACTGCGACGACATTAACAAAGGCAACT 960

RESULT 15
AA253690
ID AA253690 standard; DNA; 963 BP.
XX
AC AA253690;
XX
DT 21-MAR-2000 (first entry)
XX
DE *Neisseria meningitidis* ORF 406 partial DNA sequence SEQ ID NO:1329.
XX
KW *Neisseria meningitidis*; *Neisseria gonorrhoeae*; antigen; vaccine;
KW antigenic; diagnosis; immunogenic; infection; meningitis; septicemia;
KW antibacterial; gene therapy; ds.
XX
OS *Neisseria meningitidis*.
XX
EN W0957280-A2.
XX
PD 11-NOV-1999.
XX
PF 30-APR-1999; 99WO-US009346.
XX
PR 01-MAY-1998; 98US-0083758P.
PR 31-JUL-1998; 98US-0094869P.
PR 02-SEP-1998; 98US-0098994P.
PR 02-SEP-1998; 98US-0099062P.
PR 09-OCT-1998; 98US-0103749P.
PR 09-OCT-1998; 98US-0103794P.
PR 09-OCT-1998; 98US-0103796P.
PR 25-FEB-1999; 99US-0121528P.
XX
PA (CHIR) CHIRON CORP.
PA (GENO-) INST GENOMIC RES.
XX
PI Fraser C, Galeotti C, Grandi G, Hickey E, Masignani V, Mora M;
PI Petersen J, Pizzo M, Rappuoli R, Ratti G, Scalato E, Scarselli M;
PI Tettelin H, Venter JC;
XX
DR WPI: 2000-062150/05.
DR P-PSDB; AAY74928.
XX
PT Novel *Neisseria* polypeptides predicted to be useful antigens for
PT vaccines and diagnostics.

XX Claim 7; Page 729-730; 1453bp; English.
 PS
 XX AA253015 to AA254536, AA254577 to AA254615, and AAY74253 to AAY75941
 CC represent novel *Neisseria meningitidis* and *N. gonorrhoeae* polynucleotides
 CC and polypeptides. AA254537 to AA254576 and AA254616 to AA255473 represent
 CC PCR primers used in the exemplification of the present invention. The
 CC polypeptides, the polynucleotides, antibodies and compositions of the
 CC invention can be used as vaccines, as diagnostic reagents, and as
 CC immunogenetic compositions. The polypeptides can be used in the manufacture
 CC of medicaments for treating or preventing infection due to *Neisseria*
 CC bacteria (e.g. meningitis and septicemia), to detect the presence of
 CC *Neisseria* bacteria, or to raise antibodies. They may also be used to
 CC screen for agonists or antagonists, which may themselves have use as
 CC antibacterial agents. The polynucleotides of the invention may also be
 CC used in gene therapy protocols
 XX
 SO Sequence 963 BP; 285 A; 233 C; 218 G; 227 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 1,42e-156 Length: 963
 Score: 1624.00 Matches: 315
 Percent Similarity: 99.69% Conservative: 4
 Best Local Similarity: 98.44% Mismatches: 1
 Query Match: 98.72% Indels: 0
 DB: 3 Gaps: 0
 US-10-617-835-4 (1-320) x AA253690 (1-963)
 QY 1 MetArgAlaArgLeuLeuIleProIleuPheSerValPheIleLeuSerAlaCysGly 20
 Db 1 ArgGAGACGCGCTGCTGATGACTATTCCTTTTCAGTTTATTTATTCGCCCTGCGGG 60
 QY 21 ThrLeuThrGlyIleProSerHisGlyGlyLysArgPheAlaValGluGlnGluLeu 40
 Db 61 ACACGACAGGATTCATCCATCGATGCGGAGGTAAACGCTTCGCGGTCAACAAGACTT 120
 QY 41 ValAlaAlaSerAlaArgAlaAlaValLysPheMetAspLeuGlnAlaLeuHisGlyArg 60
 Db 121 GTGGCCGCTCTGCGCAGAGCTGCCCTTAAGACATGAGATTACAGGCATTACACGACGA 180
 QY 61 LysValAlaLeuTyrIleAlaThrMetGlyAspGlnGlySerGlySerLeuThrGly 80
 Db 181 AAAGTTGATTTGATGATTCATGCACTATGAGCGACAGGTTCAAGCATTTTACAGGGGCT 240
 QY 81 ArgTyrSerIleAspAlaLeuIleArgGlyGlyTyrIleAsnSerProAlaValArgThr 100
 Db 241 CGCTACTCATTTGATGACTGATTTGTCGCGAATACATTAACAGCCCTGCGCTCGTACC 300
 QY 101 AspTyrThrTyrProArgTyrGluThrThrAlaGluThrThrSerGlyGlyLeuThrGly 120
 Db 301 GATTACACCTATCCAGCTTACGAACCAACCGCTGAACACATCAGCGGTTTGACAGGT 360
 QY 121 LeuThrThrSerLeuSerThrLeuAsnAlaProAlaLeuSerArgThrGlnSerAspGly 140
 Db 361 TTAACCACTTCTTATCTACACTTAATGCCCTGCACTCGCGCAACCAATCAGACCGT 420
 QY 141 SerGlySerArgSerSerLeuGlyLeuAsnIleGlyGlyMetGlyAspTyrArgAsnGlu 160
 Db 421 AGCGGAATTAAGAGAGCTGGGCTTAATATGCGCGGATGGGGAATTATCGAATGAA 480
 QY 161 ThrLeuThrThrAsnProArgAspThrAlaPheLeuSerHisLeuValGlnThrValPhe 180
 Db 481 ACCTTGACGACTAAACCCGCGCACACTGCTTTCTTCCCACTTGCTACAGACCGTATTT 540
 QY 181 PheLeuArgGlyIleAspValValSerProAlaAsnAlaAspThrAspValPheIleAsn 200
 Db 541 TTCCTGCGCGGATAGAGCTGTCTCTCGCAATGCCGATACGAGATGTTTATTAAAC 600
 QY 201 IleAspValPheGlyThrIleArgAsnArgThrGluMetHisLeuTyrAsnAlaGluThr 220
 Db 601 ATCGACGATTCGGAACGATACGCAACGAACCAATGCACTTATACATGCCGAAACA 660

QY 221 LeuLysAlaGlnThrLysLeuGluTyrPheAlaValAspArgThrAsnLysLeuLeu 240
 Db 661 CTGAAGCCCAACAAACCTGAAATATTTCCAGATAGACAGAACCAATAAATAATTGCTC 720
 QY 241 IleLysProLysThrAsnAlaPheGluAlaAlaTyrLysGluAsnTyrAlaLeuTyrMet 260
 Db 721 ATCAACCAAAADACCAATGCGTTTGAAGCTGCTCTATTAAGAAAATTACGATTGGATG 780
 QY 261 GlyProTyrLysValSerLysGlyIleLysProThrGluGlyLeuMetValAspPheSer 280
 Db 781 GGACCGTATTAAGTAAGCAAGAAATTAACCGACAGAAAGATTATATGTCGATTTCTCC 840
 QY 281 AspIleArgProTyrGlyAsnHisThrGlyAsnSerAlaProSerValGluAlaAspAsn 300
 Db 841 GATATCCAAACCATACGGCAATCATATGGATACCTGCCCCATCCGATAGAGGCTGATAAC 900
 QY 301 SerHisGluGlyTyrGlyTyrSerAspGluAlaValArgGlnHisArgGlnGlyGlnPro 320
 Db 901 AGTCATGAGGGGTATGATTCAGCGATGAACAGATGCGACGACATAGACAAAGGCACT 960

Search completed: August 19, 2005, 01:04:08
 Job time : 546 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - nucleic search, using frame_plus.p2n model

Run on: August 18, 2005, 22:53:39 ; Search time 3122 Seconds
(without alignments)
3901.527 Million cell updates/sec

Title: US-10-617-835-4

Perfect score: 1645

Sequence: 1 MRARLRILPILSVFLLSACG.....SHEGYGSDAVRQHQRCOP 320

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+g2n.model -DEV=xlp
-O=/cgn2.1/USPD0001.p/US10617835/runat.18082005.115608.8376/app_query.fasta_1.519.
-DB=EST -QFMT=FASTAP -SUFFIX=p2n.rst -MINMATCH=0.1 -LOOPEL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS-human40.cdi -LIST=45
-DOCLIGN=200 -THR SCORE=PCT -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pct -NORM=EXT -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
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-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPLOCK=100 -LONGLOC
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

EST: +
1: gb_est1: +
2: gb_est2: +
3: gb_hic: +
4: gb_est3: +
5: gb_est4: +
6: gb_est5: +
7: gb_est6: +
8: gb_gsa1: +
9: gb_gsa2: +

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	104	6.3	750	5	BP182164
2	103.5	6.3	557	8	BM819564 K-EST0087
3	101	6.1	724	8	BH515144 BQGS41TF
4	100.5	6.1	853	7	CF683309 CCAB21TF
5	100.5	6.1	882	7	CF687616 CCAC089TF
6	100.5	6.1	898	7	CF701318 CCAR073TO
7	100.5	6.1	2651	9	AY412499 Mus muscu
8	100.5	6.1	4036	3	AK049496 Mus muscu
9	97.5	5.9	638	4	BI543281 S1C_G08 S

C 10	97.5	5.9	808	7	CF720552	CF720552 CCAH127TF
C 11	97.5	5.9	875	7	CF224113	CF224113 AGENCOURT
C 12	97	5.9	1074	6	CA066694	CA066694 SCEQAD101
C 13	96	5.8	800	8	BZ517711	BZ517711 BOMR19TF
C 14	95.5	5.8	553	8	CA192949	CA192949 SCRLS104
C 15	94.5	5.7	568	8	BH887997	BH887997 LB01788A.
C 16	94.5	5.7	631	1	AL961261	AL961261 AL61261
C 17	94.5	5.7	661	1	AL629935	AL629935 AL629935
C 18	94.5	5.7	902	7	CN510835	CN510835 AGENCOURT
C 19	94	5.7	688	5	BQ578598	BQ578598 WHE0307.C
C 20	94	5.7	813	7	CK200430	CK200430 FGAS00894
C 21	94	5.7	1128	9	CL977717	CL977717 OaIFC030
C 22	93.5	5.7	862	7	CN209233	CN209233 Tor9747 G
C 23	93.5	5.7	1165	6	CD508628	CD508628 CDA91-H08
C 24	93.5	5.7	1349	8	CL648116	CL648116 CH213-162
C 25	93.5	5.7	1388	8	BZ576008	BZ576008 m8h2-4730
C 26	93	5.7	581	5	BP255245	BP255245 BP255245
C 27	93	5.7	797	7	CN509047	CN509047 AGENCOURT
C 28	93	5.7	884	7	CN502363	CN502363 AGENCOURT
C 29	93	5.7	932	7	CN510402	CN510402 AGENCOURT
C 30	92.5	5.6	669	7	CF684102	CF684102 CCAGY30TF
C 31	92.5	5.6	801	6	CB904901	CB904901 LrIC040Xg
C 32	92.5	5.6	801	7	CF876129	CF876129 LrIC040Xg
C 33	92.5	5.6	847	7	CK352302	CK352302 AGENCOURT
C 34	92.5	5.6	879	7	CN507579	CN507579 AGENCOURT
C 35	92.5	5.6	1052	3	CNS0958N	BO66091 Single re
C 36	92.5	5.6	1098	9	CNS05EXB	BO55827 Single re
C 37	92.5	5.6	1206	9	CL965795	ALJ34280 Tetradon
C 38	92.5	5.6	491	2	BE106299	CL965795 OaIFC012
C 39	92	5.6	491	2	BE106299	BE106299 UI-R-B01-
C 40	92	5.6	677	3	BI471703	BI471703 aa62f03.
C 41	92	5.6	751	5	BX925187	BX048120 Single re
C 42	92	5.6	827	5	BU105657	BX925187 BX925187
C 43	92	5.6	831	6	CA487870	BU105657 603004222
C 44	92	5.6	833	2	AW982176	CA487870 AGENCOURT
C 45	92	5.6	833	2	AW982176	AW982176 HVSMBG000

ALIGNMENTS

RESULT 1
BP182164 750 bp mRNA linear EST 14-OCT-2003
, LOCUS
DEFINITION BP182164 NRPG Bombyx mori cDNA clone NRPG0202, mRNA sequence.
ACCESSION BP182164
VERSION BP182164.1 GI:37662855
KEYWORDS
SOURCE
ORGANISM Bombyx mori (domestic silkworm)

Bombyx mori
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Preyigota;
Neoptera; Endopterygota; Lepidoptera; Glossata; Dityria;
Bombycoidea; Bombycidae; Bombyx.
1 (bases 1 to 750)
Mita,K., Morimyo,M., Shimada,T., Okano,K. and Maeda,S.
Bombyx mori cDNA
Unpublished (2000)
Contract: Mita K
Genome Research Group
National Institute of Agrobiological Sciences
Owashi 1-2, Tsukuba, Ibaraki 305-8634, Japan
Email: kmite@nias.affrc.go.jp
method: uni-directional, sequence direction: sequenced from T3 primer
(5' -> 3').

FEATURES

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Location/Qualifiers
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/dev_stage="adult"
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/normalize library"
ORIGIN

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Best Local Similarity:	22.12%
Query Match:	6.32%
DB:	5
Length:	750
Matches:	50
Conservative:	27
Mismatches:	95
Indels:	54
Gaps:	7

US-10-617-835-4 (1-320) X BP182164 (1-750)

QY	116	ProLeuPheSerValPheLeuSerAlaCysGlyThrThrLeuThrGlyLeuPro	26
	127	ATTCAATTGACAAACACATCTTTCAGACAGCATCCCGCGCTACGCTGACAGTCTC	186
QY	27	SerHisGlyGlyLeuValThrPheAlaValGlnGlnGluLeuValAlaAlaSerAlaArg	46
DB	187	ACT-----	222
QY	47	AlaAlaValAlaAspMetAspLeuGlnAlaLeuHisGlyArgValAlaLeuTyrlle	66
DB	223	TCGCGA-----	255
QY	67	AlaThrMetGlyAspGlnGlySerGlySerLeuThrGlyGlyArgTyrSerIleAspAla	86
DB	256	GTCGACAGCCAGACCGCGGCGCGGCGCGCTGTCGACGCGGCATGTGCTACCGCGGCGG	315
QY	87	LeuIleArgGlyGlyTyrTrpLeuSerProAlaValArgThrAsp-----	101
DB	316	CAATATCGCGGCGCGCGCAGCATGTGCGCGGCGCTATACGCCGACGCCCTGCGCTAC	375
QY	102	-----TyrThr-----TyrProArgTyrGlnThr	109
DB	376	CCGCGCGCTCAGCGCCAGCTTACACGGCGGCGCCCTAGCCCTTACAGCGCGCACAGTAC	435
QY	110	ThrAlaGlnThrThrSerGlyGlyLeuThrGlyLeuThrThrSerLeuSerThrLeuAla	129
DB	436	ACGGCGGCACATGGCGCGTGGCGGTGCGCGCGGTACCGGTACGCGTGGCCACACCGACGG	495
QY	130	AlaProAlaLeuSerArgThrGlnSerAspGlySerGlySerArgSerSerLeuGlyLeu	149
DB	496	TCGCCGCGT-----	528
QY	150	AsnIleGlyGlyMetGlyAspTyrArgAsnGlnThrLeuThrThrAsnPro-----	166
DB	529	AACACCGCGCTCGGGCGGGAACCTCGCTCGACGCTCAAGCATGGCGCGCGCTCCACCG	588
QY	167	-----ArgAspThrAlaPheLeuSerHisLeuValGlnThrValPhePhe	181
DB	589	GCATCTTCGCGCTCCACATCGCGCGCGCGCGCTTACAGCACTGACCGGCACCAATCTTTAC	648
QY	182	LeuArgGlyIleAspValValSerProAlaAsnAlaAspThrAspAlaPheIleAsnIle	201
DB	649	ATTCGAGGACTG-----	699
QY	202	AspValPheGlyThrIle	207
DB	700	CAATGTATGCGACGACATA	717

RESULT 2

[illegible]

3, ILIRINA Sequencer.

VERSION BM819564.1 GT:19175977

KEYWORDS EST.

Hollis Bapirelis (Mullali)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE	1 (bases 1 to 557)
AUTHORS	Kim, N. S., Hahn, Y., Oh, J. H., Lee, J. Y., Ahn, H. Y., Chu, M. Y., Kim, M. R.

TITLE 21C Frontier Korean EST Project 2001
JOURNAL Unpublished (2002)

FEATURES

Source

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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon.9606"
/clone="S19N665307-8-E06"
/sex="M"
/lab_host="Top10F"
/clone_1ib="S19N665307"
/notes="Organ: Stomach; Vector: pCNS; Site.1: EcoRI;
Site.2: NotI; The poly (A)+ RNA was dephosphorylated with
bacterial alkaline phosphatase (BAP) and then deapped
with tabacco acid pyrophosphatase (TAP) . The deapped
inact mRNA was ligated with DNA-RNA linker including EcoRI
I site by treatment of T4 RNA ligase and the first strand
cDNA was synthesized from oligo dt-selected mRNA by
priming with dt-tailed vector. The dt-tailed vector was
adjusted to have about 60nt. The cDNA vector was
circularized with E. coli DNA ligase after digestion of
EcoRI which site is also included in vector. An RNA strand
converted to a DNA strand by Okayama-Berg method. The
obtained cDNA vectors were used for transformation of
competent cells E. coli Top10F by electroporation method.
The cDNA libraries constructed by this method are
full-length enriched cDNA library."

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ORIGIN

Alignment Scores:	
Pred. No.:	0.274
Score:	103.50
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Best Local Similarity:	29.76%
Query Match:	6.29%
DB:	4
Length:	55
Matches:	50
Conservative:	25
Mismatches:	58
Indels:	37
Gaps:	7

US-10-617-835-4 (1-320) X BM819564 (1-557)

[illegible]


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QY 190 ProAlaAsnAlaAspThrAspValPheIleAsnIleAspValPheGlyThrIleArgAsn 209
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QY 210 ArgThrGluMetHisLeuTyxAsnIleGluThrLeuValGlnThrLeuGluTyr 229
Db 407 CGCGGCG-----GTTGCCGACACCAATGAGAACGCT 378
QY 230 PheAlaValAspArgThrAsnValLeuLeuIleValProTyrThrAsnIlePheGlu 249
Db 377 TCTGCTGTCAACTTCATTCATTCAGCTTATCCCTTCAACGCGCGCT----- 324
QY 250 AlaAlaTyrGlyGluAsnTyrAlaLeuTyrMetGlyProTyrValSerLeuGlyIle 269
Db 323 TCAGCTTTCGCGATTCACAGACAGTT-----GAGAGT 291
QY 270 LysProThrGluGlyLeuMetValAspPheSerAspIleArgProTyrGlyAsnIleThr 289
Db 290 CGAGGAATGAGATCGCTTGTAGGGGATTTTAGACAGCTAATTGTAGCGGACAGGAGC 231
QY 290 GlyAsnSerAlaProSerValGluAlaAspAsnSer 301
Db 230 ATAAACCTCTCTCCAAAGGTTGCAACGACGACAGTAC 195
RESULT 6
CF701318/c 898 bp mRNA linear EST 16-AUG-2004
LOCUS CCAFO7370 C.neoformans strain JEC21 Cryptococcus neoformans var.
ACCESSION CF701318
VERSION CF701318.1 GI:41555477
KEYWORDS EST
SOURCE Cryptococcus neoformans var. neoformans (Filobasidiella neoformans
var. neoformans)
ORGANISM Cryptococcus neoformans var. neoformans
Bukaryota; Fungi; Basidiomycota; Hymenomycetes;
Heterobasidiomycetes; Tremellomycetidae; Tremellales; Tremellaceae;
Filobasidiella.
REFERENCE 1 (bases 1 to 898)
AUTHORS Loftus,B.
TITLE End sequencing of clones from a full length enriched, normalized
JOURNAL JEC21 cDNA library
COMMENT Unpublished (2003)
Other_ESTs: CCAFO737R
CONTACT: Brendan Loftus
TIGR
Department of Bukaryotic Genomics, TIGR, 9712 Medical Center Drive,
Rockville, MD 20850, USA
Tel: 301-838-3543
Fax: 301-838-0208
Email: crypt@tigr.org
Seq primer: TP.
FEATURES
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1..898
Location/Qualifiers
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/mol_type="mRNA"
/strain="JEC21"
/db_xref="taxon:40410"
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/notes="Vector: pCMVSPORT6; Site 1: NotI EcoRV; The full
length, normalized library was prepared from a variety of
conditions using RNA provided by Joseph Heitman and
Jenniffer Lodge"
ORIGIN
Alignment Scores:
Pred. No.: 1.25 Length: 898
Score: 100.50 Matches: 57
Percent Similarity: 35.328 Conservative: 32
Best Local Similarity: 22.624 Mismatches: 88
Query Match: 6.11% Indels: 75
DB: 7 Gaps: 10

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US-10-617-835-4 (1-320) x CF701318 (1-898)
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Db 821 GGCGCTTATCGTAATATATCCCTCTGCTGCTCCGATCT-----GCTTATGAGGC 768
QY 110 ThrIleGluThrThrSerGlyGlyLeuThr----- 119
Db 767 AACGCTGGCTTACCTCGGACATATCTCCGCCACATGAGTCCGACGAGTATGCG 708
QY 120 -----GlyLeuThrThrSerLeuSer----- 126
Db 707 CAACAGAACTCGGAAGAAATTGGCTCCGGTTTGGGATCTCAGCAATTGGGGCTAGC 648
QY 127 -----ThrLeuAsnAlaProAlaLeu 133
Db 647 TAGATCCAGGCTGACGCGAGTGGGATGCGGATGAGCATCTCAGACCTTCAAGT 588
QY 134 SerArgThrGlnSerAspGlySerGlySerSerSerLeuGlyLeuAsnIleGly---- 152
Db 587 TTGAGAGCTCAGAGTCACAGGAGACCTCGGCTTCACTGTCGGACCGAATCTGTGTT 528
QY 153 -----GlyMetGlyAspTyrArgAsnGluThrLeuThrThrAsnProArgAspThr 169
Db 527 CCGCTCGGCTGGCTGAGGTTCTTCAAGAGGAGAGCTTTGCA-----CCATTGATGCG 474
QY 170 AlaPheLeuSerHisLeuValGlnThrValPhePheLeuArgGlyIleAspValIleSer 189
Db 473 GCGCCTATTCATCCTCTTCCAAAGCTGTC-----GGCATTCAGATGTGTAGCG 426
QY 190 ProAlaAsnAlaAspThrAspValPheIleAsnIleAspValPheGlyThrIleArgAsn 209
Db 425 CGAGCTCCTGGT-----TCATTTGAGAGCCTTGGTTTACACCCCAT 384
QY 210 ArgThrGluMetHisLeuTyxAsnIleGluThrLeuValGlnThrLeuValSerLeuGluTyr 229
Db 383 CGCGGCG-----GTTGCCGACACCAATGAGAACGCT 354
QY 220 PheAlaValAspArgThrAsnValLeuLeuIleValProTyrThrAsnIlePheGlu 249
Db 353 TCTGCTGTCAACTTCATTCATTCAGCTTATCCCTTCAACGCGCGCT----- 300
QY 250 AlaAlaTyrGlyGluAsnTyrAlaLeuTyrMetGlyProTyrValSerLeuGlyIle 269
Db 299 TCAGCTTTCGCGATTCACAGACAGT-----GAGAGT 267
QY 270 LysProThrGluGlyLeuMetValAspPheSerAspIleArgProTyrGlyAsnIleThr 289
Db 266 CGAGGAATGAGATCGCTTGTAGGGGATTTTAGACAGCTAATTGTAGCGGACAGGAGC 207
QY 290 GlyAsnSerAlaProSerValGluAlaAspAsnSer 301
Db 206 ATAAACCTCTCTCCAAAGTTCACAGCAGCAGTAC 171
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LOCUS AY412499
DEFINITION Mus musculus HCM4577 gene, VIRUTAL TRANSCRIPT, partial sequence,
ACCESSION AY412499
VERSION AY412499.1 GI:39768464
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 2651)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejririwal,A.,
Todd,M.A., Tanenbaum,D.M., Civallo,D.R., Lu,F., Murphy,B.,
Fertiera,S., Wang,G., Zheng,X.H., White,T.D., Slnsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous

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JOURNAL	Gene	trios
REFERENCE	Science	302 (5652), 1960-1963 (2003)
PUBMED	14671302	
AUTHORS	2 (bases 1 to 2651)	
	Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,	
	Todd,M.A., Tanenbaum,D.M., Ciavella,D.R., Lu,F., Murphy,B.,	
	Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,	
	Adams,M.D. and Cargill,M.	
TITLE	Direct Submission	
JOURNAL	Submitted (16-NOV-2003)	Celera Genomics, 45 West Gude Drive,
	Rockville, MD 20850, USA	
COMMENT	This sequence was made by sequencing genomic exons and ordering	
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ORIGIN	/locus_tag="HGM4577"	
Alignment Scores:		
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Score:	100.50	Matches: 50
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Best Local Similarity:	25.00%	Mismatches: 63
Query Match:	6.11%	Indels: 59
DB:	9	Gaps: 11
US-10-617-835-4 (1-320) x AY412499 (1-2651)		
Oy	76 SerleuThrGlyGly-	-----ArgTyrSerIleAspAlaLeu 87
Db	1413 ACTCGACTTCGCCGGAACACACACCGAAGCGATACACCGGTACCTTGATGCACC	1472GATGCACC
Oy	88 Ile-----ArgGlyGluTyrIleAsnSerProIaValArgThrAspTyrThrTyrPro	105
Db	1473 GTATCCTCTCCGACACAGCTACCGAAGAAACCCCTTGAGAGCTCAAGTAT	-----1523
Oy	106 ArgTyrGluThrThrAlaGluThrThrSerGlyGlyLeuThrGlyLeuThrThrSerIleu	125
Db	1534 -----TCTCGCAGAGGTGGTAC	-----CTC 1544
Oy	126 SerThrIleuAsnAlaProIaLeuSerArgThrGlnSerAspGlySerGlySerArgSer	145
Db	1545 AGCGACGGAGACTCACCCGAACCTG--AGAACTAGATCTAGCAAGCATGATCGGAGCAC	1601
Oy	146 SerIleuGly-	-----IleuAsnIle 151
Db	1602 AAACCTGGGAAAAGGAGAGAAACTGTCCCAAGCACTGTAGCAAAAATGAACTAGACATC	1661
Oy	152 GlyGlyMetGlyAspTyrArgAsnGluThrIleuThrThrAsnProArgAspThrAlaPhe	171
Db	1662 GTGGCC-----TTCAGACATATACAGCTTTGGGATCAACCAATATGTCGCGAGTAC	1712
Oy	172 LeuSerHisIleuValGlnThrValPhePheLeuArgGlyIleAspValIaSerProIa	191
Db	1713 ATATTCGGCCCTTCATAGAGGTACACTTCAT-----GGAGCTGAGGGTTTAAACCGGCC	1766
Oy	192 AsnAlaAspThr--AspValPheIleAsnIleAspValPheGlyThrIleArgSerAsn	210
Db	1767 CGGATAGATTGGAAGAAGATGTGTTTGTGCCATTTCAGTGNAGCTCAGTGAACAAACCGA	1822
Oy	211 ThrGluMet-----HisIleuTyrAsnAlaGlu	219
Db	1827 ACGGCTGCTCACCTGTCCGACGACCTTCTTAGCATGACACACACCTTCAACATAGAG	1888
Oy	220 ThrIleuValaGln--ThrIleuGluTyrIlePheAlaValaAspArgThrAsnIleu	238
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LOCUS	AKO49496	4036 bp	mRNA	linear	HTC 03-APR-2004
DEFINITION	Mus musculus 7 days embryo whole body cDNA, RIKEN full-length enriched library, clone: C430017H6 product: weakly similar to THR101000381 PROTEIN (FRAGMENT) [Homo sapiens], full insert sequence.				
ACCESSION	AK049496				
VERSION	AK049496.1 GI:26340229				
KEYWORDS	HTC; CAP trapper.				
SOURCE	Mus musculus (house mouse)				
ORGANISM	Mus musculus				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
AUTHORS	Carninci, P. and Hayashizaki, Y.				
TITLE	High-efficiency full-length cDNA cloning				
JOURNAL	Meth. Enzymol. 303, 19-44 (1999)				
MEDLINE	99279253				
PUBMED	10349636				
REFERENCE	2				
AUTHORS	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.				
TITLE	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes				
JOURNAL	Genome Res. 10 (10), 1617-1630 (2000)				
MEDLINE	20499374				
PUBMED	11042159				
REFERENCE	3				
AUTHORS	Shibata, K., Itoh, M., Aizawa, K., Nagao, S., Sasaki, N., Carninci, P., Kono, H., Akiyama, J., Nishi, K., Kitanai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakauechi, S., Ikegami, T., Kashiwagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Wataniki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsumura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.				
TITLE	RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer				
JOURNAL	Genome Res. 10 (11), 1757-1771 (2000)				
MEDLINE	20530913				
PUBMED	1107661				
REFERENCE	4				
AUTHORS	The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.				
TITLE	Functional annotation of a full-length mouse cDNA collection				
JOURNAL	Nature 409, 685-690 (2001)				
REFERENCE	5				
AUTHORS	The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.				
TITLE	Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs				
JOURNAL	Nature 420, 563-573 (2002)				
REFERENCE	6 (bases 1 to 4036)				
AUTHORS	Aadachi, J., Aizawa, K., Akimura, T., Arai, A., Hashizume, W., Fukuda, S., Furuno, M., Hanagaki, T., Haru, A., Hashizume, W., Hayashizaki, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imoto, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Kono, H., Kouda, M., Koyu, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numa, R., Ohno, M., Ohnato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sobabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yaeunishi, A., Yutani, M. and Hayashizaki, Y.				
TITLE	Direct Submission				
JOURNAL	Submitted (16-JUL-2001) Yoshihide Hayashizaki. The Institute of Physiological and Chemical Research (RIKEN), Laboratory for Genome Exploration and Chemical Research, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gs.c.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)				
COMMENT	cDNA library was prepared and sequenced in Mouse Genome				

Encyclopedic Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN,
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.

Please visit our web site for further details.
URL: <http://genome.sgc.riken.jp/>
URL: <http://gantom.sgc.riken.jp/>.

FEATURES

Bouice

```

/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
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/db_xref="taxon:10090"
/clone="C430017H16"
/tissue_type="whole body"
/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev_stages="7 days embryo"
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polyA_signal 4009. 4014
              /note="putative"
polyA_site   4036
              /note="putative"
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ORIGIN

Alignment Scores:	
Pred. No.:	11.9
Score:	100.50
Percent Similarity:	39.00%
Best Local Similarity:	25.00%
Query Match:	6.11%
DB:	3
Length:	403
Matches:	50
Conservative:	28
Mismatches:	63
Indels:	11
Gaps:	19

US-10-617-835-4 (1-320) X AK049496 (1-4036)

Qy	76	SerLeuThrGlyGlyL-----ArgTyrSerIleLeuAlaLeu	87
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Db	1442	ACTCTGACTTCCGGGAAACCCAGCAAGCTGATTAAGCCGTATCATCTTATATACACC	1501
Qy	88	Ile-----ArgGlyGluTyrIleLeuSerProAlaValArgThrAspTyrThrTyrPro	105
		::: :::	
Db	1502	GATTCCTCTCGGCACACGCTACCGGAGAAACCCCTTGGAGCTCGAAGTAT-----	1552
Qy	106	ArgTyrGluThrThrAlaGluThrThrSerGlyGlyLeuThrGlyLeuThrThrSerLeu	125
		:::	
Db	1553	-----TCTCGCAAGGCTGGGTAC-----CTC	1572

Oy	126	SerThrIeuAaNIaAProAlaLeuSerArgThrGlnSerAspGlySerGlySerArgSer	145
Db	1574	AGCCAGCGAGACTACCCGAATCG---AGAACTAGATCTACGACAGCATGATCGGAGCAC	1633
Oy	146	SerLeuGly-----LeuAaNIaLe	151
Db	1631	AAACTTGAGAAAGGAGAGAAATCTGTCCCAAGCAGTGTGACAAAATAAGACTTAGACATTC	1699
Oy	152	GlyIleuSerGlyAspTyrArgAsnGlyIuThrIeuThrIAsnProArgAspThrAlaPhe	171
Db	1691	GGTCC-----TTCAGACATTACAGCTTGGCATCAACCCAAATGCTCGCAGATAC	1741
Oy	172	LeuSerHisIeuValGlnThrValPhePheIeuArgGlyIleAspValIserProAla	191
Db	1742	ATATCTCGGCTCATAGAGCGTACCTTCTAT-----GGAGCTGAGGGTTTAAACCCGCC	1799
Oy	192	AsnAlaAspThr---AspValPheIleAsnIleAspValPheGlyThrIleArgAsnArg	210
Db	1796	CGGATGATGTTCGAAGAAGATGCTTTTGTCGCAATTCAGGTAGACCTAGTAAACAAAGCAGA	1855
Oy	211	ThrGluMet-----HisIeuTyrAsnAlaGlu	219
Db	1856	ACGGCCCTGCTCACCTGTGCGAGCACCTTCTTAGACATGAGCACACACCTTAAACATTAAG	1915
Oy	220	ThrIeuTyrAlaGln---ThrIleuGlnIuTyrPheAlaValaLapArgThrAsnIleValys	238
Db	1916	ATTGAAAAATGGCAGCATCTGAGCTGGTGTGTTCACCTGGAGCCACCGCCGAGGAGG	1977

RESULT 9
BI543281

BI543281

DEFINITION

LOCUS	638 bp	mRNA	linear	EST 04-SEP-2001
DEFINITION	B1543381			
	SIC_G08 Sugar Beet stress germination cDNA library (subtracted)			
	Beta vulgaris cDNA 5' similar to xyloglucan			
	endo-1,4-beta-D-glucanase, mRNA sequence.			

ACCESSION

VERSION BI543281.1 GI:15427459

KEYWORDS

SOURCE	Beta vulgaris (sugar beet)
--------	----------------------------

ORGANIT

Eukaryota; Viridiplantae;

Caryophyllales; Amaranthaceae; Beta.

REFERENCE

AUTHORS de los Reyes, B.G., McGrath, J.M., Myers, S. and Derrico, C.

TITLE

vulgaris) germinated under stress conditions

JOURNALS

COMMENT
Contact: J. Mitchell McGrath

Unit
with a... Create... Information...

MICHIGAN STATE UNIVERSITY
494 Plant and Soil Sci. Bldg., East Lansing MI 48824, USA
Tel.: 517 353 0000

Tel: 31 / 333 9262
Fax: (517) - 337-6782

Email: mitchmc@msu.edu

Seq primer: T3.

FEATURES

Source

```

/organism="Beta vulgaris"
/mol_type="mRNA"
/cultivar="USH20"
/db_xref="taxon:161934"
/tissue_type="whole seedlings"
/dev_stage="4-day germination under stress (salt/NaCl, osmotic/Mannitol)"
/lab_host="XLI-Blue MRF"
/lab_host="Sugar Beet stress germination cDNA library (subtracted)"
/notes="Organ: seeds; Vector: pBluescript II KS (+); Site_1: EORI, Site_2: XhoI; The mRNA samples used for this library were derived from seedlings germinated for 4 days in 150mM NaCl and 200mM mannitol. The mRNA pool

```

used as template for double stranded cDNA synthesis using the Stratagene Bluescript XR cDNA synthesis and library kit. The resulting cDNA was used as a tester for subtraction against a driver cDNA population derived from 4-day old seedlings germinated in moist filter paper. Subtraction was performed using the Invitrogen Photobiotin-Streptavidin subtractor kit. The cDNA library was generated by directional ligation of the subtracted cDNAs in the EcoRI and XhoI sites of pBluescript XR vector (Stratagene). "

ORIGIN

Alignment Scores:

Pred. No.:	1.68	Length:	638
Score:	97.50	Matches:	48
Percent Similarity:	37.07%	Conservative:	28
Best Local Similarity:	23.41%	Mismatches:	68
Query Match:	5.93%	Indels:	61
DB:	4	Gaps:	10

US-10-617-835-4 (1-320) x B1543281 (1-638)

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Qy 24 GYIIEProSerHISGlyGlyValArgPheAlaValGluGlnGln----- 39
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Db 23 GGACTTCATCAAAATGGGGACATGAGGTGCTGTGTGACCTCAATTATATGTTG 82
Qy 40 -----LeuValAlaAlaSerAlaArgAlaAla---ValLysAspMetAspLeuGln 55
    :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 83 CTATATTCATGATGAGGACATGACTGATGTCATGATGTCATGATGATGATGATG 142
Qy 56 AlaleuHISGlyGlyValAlaAlaLeuValArgPheAlaValGluGlnGln 75
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 143 ACTTTGGAGGTGAGGAGGTCAAAACATAT-----GGTTGGGGT 181
Qy 76 -----SerLeuThrGlyValArgGlySerIleAspAlaLeuIleArgGlyGlu 91
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 182 GGTGATCATCTCTCGCTCTCATAGACCATGACTCT-----GGATCC 223
Qy 92 TyrIleAsnSerProAlaValArgThrAspTyrThrTyrProArgTyrGluThrAla 111
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 224 GGCCTCACCTCC-----AAAAAGACCTTATTTATTTGGAGATTTGATGCAATG 274
Qy 112 GluThrThrSerGlyGlyLeuThrGlyLeuThrThrSerLeuSerThrLeuAsnAlaPro 131
    :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 275 AAACCTGCTGCTGATCACTGACGACCTGCTCATCTTTATTTGCAATCGACCT 334
Qy 132 AlaleuSerArgThrGln-----SerAspGlySerGlySerArg 144
    :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 335 AGCACTGGTACATGACGATGACATGCTTGTGATTTAGAAATGCCAGTGACAGCT 394
Qy 145 SerSerLeuGlyLeuAsnIleGlyGlyMetGly----- 155
    :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 395 TACACCTCCACACCAACGATGTTGGCGAAGGAAAGGAGATGAGGACAGCATTCGA 454
Qy 156 -----AspTyrArgAsnGluThrLeuThrThrAsnProArg--- 167
    :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 455 CTCTGCTTGAACCAACCAATGAATACCAACCTTATTCATTTGGAACCCGAGATC 514
Qy 168 -----AspThr-----AlaPheLeuSerHisLeuValGlnThr 178
    :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 515 ATCATGTTCTTGTCGATGAATAACACCAATTAAGATATTTTAACCATGAGAAACACGGA 574
Qy 179 ValPhePheLeuArg 183
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Db 575 GTTCTCTTCTTAAG 589

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RESULT 10
 CF720552/c 808 bp mRNA linear EST 16-AUG-2004
 LOCUS CCAH127Tf C.neoformans strain JEC21 Cryptococcus neoformans var.
 DEFINITION CCAH127Tf C.neoformans strain JEC21 Cryptococcus neoformans var.
 ACCESSION CF720552
 VERSION CF720552.1 GI:41574711

KEYWORDS EST.
 SOURCE Cryptococcus neoformans var. neoformans (Filobasidiella neoformans var. neoformans)

ORGANISM

Cryptococcus neoformans var. neoformans
 Eukaryote; Fungi; Basidiomycota; Hymenomycetes;
 Heterobasidiomycetes; Tremellomycetidae; Tremellales; Tremellaceae;
 Filobasidiella.
 1 (bases 1 to 808)

REFERENCE
 Loftus,B.
 End sequencing of clones from a full length enriched, normalized

TITLE

JEC21 cDNA library

JOURNAL

Unpublished (2003)

Other ESTs: CCAH127Tf

Contact: Brendan Loftus

TIGR

Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,

Rockville, MD 20850, USA

Tel: 301-838-3543

Fax: 301-838-0208

Email: crypt@tigr.org

Seq primer: TF.

Location/Qualifiers

1..808

/organism="Cryptococcus neoformans var. neoformans"

/mol_type="mRNA"

/strain="JEC21"

/db_xref="taxon:40410"

/clone="CCAHI27"

/note="Vector: pCMVSPORT6; Site_1: NotI EcoRV; The full

length, normalized library was prepared from a variety of

conditions using RNA provided by Joseph Heitman and

Jennifer Lodge"

DB:

US-10-617-835-4 (1-320) x CF720552 (1-808)

ORIGIN

Alignment Scores:

Pred. No.:	2.39	Length:	808
Score:	97.50	Matches:	57
Percent Similarity:	34.92%	Conservative:	31
Best Local Similarity:	22.62%	Mismatches:	89
Query Match:	5.93%	Indels:	75
DB:	7	Gaps:	10

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Qy 90 GYIuTyrIleAsnSerProAlaValArgThrAspTyrThrTyrProArgTyrGluThr 109
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 783 GGCCTTATGTAATATATCCCTGCTGCTGCTGCCGATTT-----GCTTATGAGGC 730
Qy 110 ThrIleGluThrThrSerGlyGlyLeuThr----- 119
    :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 729 AAGCTGCTTACCTCGGACATATCTCCGCCCACTGATCCGACGAGATGTATGCG 670
Qy 120 -----GlyLeuThrThrSerLeuSer----- 126
    :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 669 CACTGGAATCGCAAAAGAAATGGCTCCGTTGGAGTCTGCAATGTGGGCTAAGC 610
Qy 127 -----ThrLeuAsnAlaProAlaLeu 133
    :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 609 TACATCCAAAGCTGCACGCGAGTGGGATATGCCATGACATGTGAGACCTTCAAGT 550
Qy 134 SerArgThrGlnSerAspGlySerGlySerArgSerLeuGlyLeuAsnIleGly--- 152
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 549 TTGAGAGTCAAGACTGACAGAGGAGACTCGGCTTCACTGTCGAGACGAAATCTTGCTGT 490
Qy 153 -----GlyMetGlyAspTyrArgAsnGluThrLeuThrThrAsnProArgAspThr 169
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 489 CCTGCTCGGCTGGAGTTCCTTCAAGAGGAGAGACTTTTGA-----CCATTGGATGCG 436
Qy 170 AlaPheLeuSerHisLeuValGlnThrValPhePheLeuArgGlyIleAspValSer 189
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Db 435 GCGCCTATTCATATCTCTTCCAAAGCTGTC-----GCCATTCCAGTGTGAGCG 388

```

QY 190 ProAlaAsnAlaAspThrAspValPheIleAsnIleAspValPheGlyThrIleArgAsn 209
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 Db 387 CGAGTCTCTGGT-----TCAAATGGAGCCTCTGGTTCACACCCCAT 346
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 QY 210 ArgThrGluMetHisIleuTyzAsnAlaGluThrIleuTyzAlaGluThrIleuGluTyz 229
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 Db 345 CCGCGG-----GTTGCCGACACCAATGAGAACGCT 316
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 QY 220 PheAlaValAspArgThrAsnIleuTyzIleuIleuTyzProIleuThrAsnAlaPheGlu 249
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 Db 315 TCTGCTGCAACTTATAGCCCTAGTACTCTGATCCCTTCAACGGGCGCT----- 262
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 QY 250 AlaAlaTyzIleuGluAsnIleuTyzAlaIleuTyzProIleuTyzIleuValSerIleuGly 269
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 Db 261 TCAGCTTGGCCGATACACAGCAGT-----GAGTG 229
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 QY 270 LysPheThrGluGlyIleuMetValAspPheSerAspIleArgProTyzIleuAsnIleuThr 289
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 Db 228 CGAGGAATGATGATGCTTCTAGGGATTTTACACAGCTAATGTGACGGGACAGGACG 169
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 QY 290 GlyAsnSerAlaProSerValGluAlaAspAsnSer 301
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 Db 168 ATAAACCTCTCCAAAGTTGCAACGACGACGATGAC 133
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 RESULT 11
 CF224113/c 875 bp mRNA linear EST 04-AUG-2003
 LOCUS AGENCOURT_15069986 NICHD_XGC Emb7 xenopus tropicalis cDNA clone
 DEFINITION IMAGE:6977012 5', mRNA sequence.
 CF224113
 ACCESSION CF224113
 VERSION
 KEYWORDS EST.
 SOURCE
 ORGANISM
 Xenopus tropicalis (western clawed frog)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Amphibia; Batrachia; Anura; Mesobatrachia; Pipridae; Pipidae;
 Xenopodinae; Xenopus; Silurana.
 1 (bases 1 to 875)
 NIH-MGC http://mgc.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Daniela S. Gerhard, Ph.D.
 Office of Cancer Genomics / NCI
 National Cancer Institute / NIH
 Bldg. 31 Rm10A07 Bethesda, MD 20892
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: Robert M. Grainger
 CDNA Library Preparation: Life Technologies, Inc.
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLM14631 row: b column: 19
 High quality sequence start: 22
 High quality sequence stop: 56.
 Location/Qualifiers
 1. 875
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 /mol_type="mRNA"
 /db_xref="taxon:8364"
 /clone="IMAGE:6977012"
 /release_type="embryo, stages 20-27"
 /dev_stage="embryo, stages 20-27"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NICHD XGC Emb7"
 /note="Vector: pCMV-SF06.1; Site 1: NotI; Site 2: EcoRV;
 cloned unidirectionally. Primer: Oligo dT. Average insert
 size 2.1 kb. Constructed by Invitrogen. Note: This is a
 Xenopus Gene Collection (XGC) library."

Pred. No.: 2.7 Length: 875
 Score: 57.50 Matches: 46
 Percent Similarity: 39.88% Conservatve: 21
 Best Local Similarity: 27.38% Mismatches: 70
 Query Match: 5.93% Indel: 31
 DB: 7 Gaps: 6
 US-10-617-835-4 (1-320) x CF224113 (1-875)
 QY 21 ThrIleuThrGlyIleProSerHisGlyGlyIleuTyzArgPheAlaValGluGluIleu 40
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 Db 666 TCGTTCCTTCATGATGCTGCCACGCT-----GAAAGCTGGGA 628
 |||||
 QY 41 ValAlaAsnAlaArgAlaValAlaValAspMetAspLeuGlnAlaLeuHisGlyArg 60
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 Db 627 GTGGGTGCCAGGCGCCGAGCTGACGCTCCAAATACATCTGTGTAAGCAGCTTCMAAGA 568
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 QY 61 LysValAlaLeuTyzIleAlaThrMetGlyAspGlnGlySer-----GlySerIleuThr 78
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 Db 567 AGTGTGCTCTTTCACAGAGGTGAGGCGGCGGCGGCGGCGGCGGCTTGGGGCTTCAT 508
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 QY 79 GlyIleArgTyzSerIleAspAlaLeuIleArgGlyIleuTyzIleuAsnSerProAlaVal 98
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 Db 507 GCGGCACTGCMAAGCGCAAGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCTC 448
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 QY 99 ArgThrAspTyzThrTyzProArgTyzIleuThrAlaGluThrThrSerGlyGlyIleu 118
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 Db 447 CGGACTGAA-----GCGCAACAGGCGGCGGCGGAGT 415
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 QY 119 ThrGlyIleuThrThrSerIleuSerThrIleuAsn-----AlaProAlaLeu 133
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 Db 414 GCAGGTAAAGCAACTAGTGTGTAAGCTTCATGAGGGGTGAAGAGGCTGTACACTTTCG 355
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 QY 134 SerArgThrGlnSerAspGlySerGlySerIleuGlyIleuAsnIleuGlyIleu 153
 |||||
 Db 354 -----CATGATGCTGATCAGAGCTTGGGCAACCAATCTCGGTGGC 316
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 QY 154 MetGlyAspTyzArgAsnGluThrIleuThrThrAsnPro---ArgAspThrAlaPheLeu 172
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 Db 315 GCAGACACGAGCCATGACCATCTTCGCGGCTGCCAGGTGAGGTGTGACAGTCAAT 256
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 QY 173 SerHisLeuValGlnThrValPhe 180
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 Db 255 TCTCATCTCTGACGTCCCACTTC 232
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 RESULT 12
 CA066694 1074 bp mRNA linear EST 23-SEP-2003
 LOCUS SCQAD01019F10.g AD1 Saccharum officinarum cDNA clone SCQAD01019F10
 DEFINITION 5', mRNA sequence.
 CA066694
 ACCESSION CA066694
 VERSION CA066694.1 GI:34918218
 KEYWORDS EST.
 SOURCE
 ORGANISM
 Saccharum officinarum
 Saccharum officinarum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACAD
 clade; Panicoideae; Andropogoneae; Saccharum; Saccharum officinarum
 complex.
 1 (bases 1 to 1074)
 Vettore, A.L., da Silva, F.R., Kemper, E.L. and Arruda, P.
 The libraries that made SUCESF
 Genet. Mol. Biol. 24 (1-4), 1-7 (2001)
 Contact: Arruda P
 Centro de Biologia Molecular e Engenharia Genetica
 Universidade Estadual de Campinas
 Caixa Postal 6010, 13083-970, Campinas SP, Brazil
 Tel: 55 19 3788 1137
 Fax: 55 19 3788 1089
 Email: partruda@unicamp.br
 Clone distribution: clone distribution information can be found
 through the Brazilian Clone Collection Center (BCCC) at
 http://www.bcccenter.fcav.unesp.br

ORIGIN
 Alignment Scores:

Plate: 019 row: F column: 10
Seq primer: T7 Promoter Primer.

FEATURES

source

Location/Qualifiers

1. 1074

/organism="Saccharum officinarum"

/mol_type="mRNA"

/db_xref="taxon:4547"

/clone="SCEAD1019F10"

/lab_host="DH10B"

/clone_lib="AD1"

/note="Organ: seedlings inoculated with Gluconacetobacter diazotrophicus; Vector: pSPori; Site_1: SalI; Site_2: NotI; An unidirectional cDNA library generated from (seedlings inoculated with Gluconacetobacter diazotrophicus). cDNA was prepared from polyA+ mRNA using Superscript Plasmid System Kit (Invitrogen). The double-strand cDNAs were fractionated in a sepharose CL-2B 40cm-columns and fragments sizing between 0.8 and 1.5 kb were directionally cloned into the vector. Details of each source of RNA and library construction can be obtained at <http://sucrest.lad.ic.unicamp.br/public>"

ORIGIN

Alignment Scores:

Pred. No.:	4.19	Length:	1074
Score:	97.00	Matches:	37
Percent Similarity:	42.52%	Conservative:	17
Best Local Similarity:	29.13%	Mismatches:	61
Query Match:	5.90%	Indels:	12
DB:	6	Gaps:	4

US-10-617-835-4 (1-320) x CA066694 (1-1074)

```

Oy 32 LysArGpHeaIaValGlucInglueValAlaIaIaSerAlaArgAlaAlaValIysAsp 51
    |||||
Db 252 AAGGCTTCAGAGGCGAGCTGACGCTGTGCTGTCCGGCGCGCGCTGTCAAG--- 308
    ::|||
Oy 52 MetAspLeuGlnAlaLeuHisGlyArgIysValAla--LeuTyrIleAlaThrMetGly 70
    ::|||
Db 309 GTGAAGACCGAGTGCATGCGAGCGGCGAGTGCATGCGCGGTAGCGTGAAGTGAAGGCC 368
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Oy 71 AspGlnGlySerGlySerLeuThrGlyArgGlySer----- 83
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Db 369 GAATCCGTCGACGAGTGTGCGGAGCCAGATCCGATGCTCTCCGCCCGCGAG 428
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Oy 84 IleAspAlaLeuIleArgGlyGluTyrIleAsnSerProAlaValArgThrAspTyrThr 103
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Db 429 GCCACGCCAAGGTGAAGAGGAGCGGACCGATTCGCCCAAGAGGCCGACCGATTC 488
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Oy 104 TyrProArgTyrGluThrThrAlaGluThrThrSerGlyGlyLeuThrGlyLeuThrThr 123
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Db 489 GTCCCCCGGCGCGCGCTGTGGGCGCGCGGCGAACCAGGCGGCTTAAAGCC 548
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Oy 124 SerLeuSerThrIleAsnAlaProAlaLeuSerArgThrGlnSerAspGlySerGlySer 143
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Db 549 CTTGATTC-----CCGCCGCGGCTTGAAAGAAAGAAAGAGGCGCTTAAGGGGAG 599
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Oy 144 ArgSerSerLeuGlyLeuAsn 150
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Db 600 AGGAACCTTTGGAGAAAGAAC 620
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RESULT 13

BZ517711

LOCUS BZ517711 800 bp DNA linear GSS 16-DEC-2002
DEFINITION BOMRT19TF_BO_2_3_KB Brassica oleracea genomic clone BOMRT19,
genomic survey sequence.

ACCESSION BZ517711

VERSION BZ517711.1 GI:27048264

KEYWORDS GSS.

SOURCE Brassica oleracea

ORGANISM Brassica oleracea
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

REFERENCE
1 (bases 1 to 800)
AUTHORS Town C.D., Van Aken S., Uterback T., Koo H. and Fraser C.M.
TITLE Whole genome shotgun sequencing of Brassica oleracea
JOURNAL Unpublished (2001)
COMMENT Other GSSs: BOMRT19TR
Contact: Chris Town
TIGR

9712 Medical Center Drive, Rockville, MD 20850, USA.
Tel: 301-838-3523
Fax: 301-838-0208
Email: cdtown@tigr.org

DNA is from a doubled haploid provided by Tom Osborn.
Seq primer: TF
Class: sheared ends.

FEATURES

source

Location/Qualifiers

1. 800

/organism="Brassica oleracea"

/mol_type="genomic DNA"

/strain="TO100DH3"

/db_xref="taxon:3712"

/clone="BOMRT19"

/clone_lib="BO_2_3_KB"

/note="Vector: pHOSt; Site_1: BstXI; 2-3 kb sheared
genomic DNA inserted into pHOSt using BstXI linkers"

ORIGIN

Alignment Scores:

Pred. No.:	3.53	Length:	800
Score:	96.00	Matches:	58
Percent Similarity:	33.96%	Conservative:	33
Best Local Similarity:	21.64%	Mismatches:	99
Query Match:	5.84%	Indels:	78
DB:	8	Gaps:	12

US-10-617-835-4 (1-320) x BZ517711 (1-800)

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Oy 41 ValAlaIaSerAlaArgAlaAlaValIysAspMetAspLeuGlnAlaLeu----- 57
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Db 26 ATGACCGCTGAGCATGCGCTCAAGTCAAGACAAAGATCCGCGGTTTCGTTGAAA 85
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Oy 58 -----HisGlyArgGlyValAlaLeuTyrIleAlaThrMetGlyAspGln 72
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Db 86 AATATTATTTCCCGCCAGCGT-----TTACATTATGATCGTTACCGATAC 133
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Oy 73 GlySerGlySerLeuThrGlyGlyArgTyrSerIleAspAlaLeuIleArgGlyGluTyr 92
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Db 134 GATTCACAGTTCATGATGAGCAAT-----TCAAGAGATTC 169
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Oy 93 IleAsnSerProAlaValArgThrAspTyrThrTyrProArgTyrGluThrThrAlaGlu 112
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Db 170 TGTGCAATGAAATTCATGACATTAAGCCCTCCACTCCTCGTTACCGCAAGT----- 223
    |||||
Oy 113 ThrThrSerGlyGlyLeuThrGlyLeuThrThrSerLeuSerThrIleAsnAlaProAla 132
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Db 224 -----AATGCCAGCA 235
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Oy 133 LeuSerArgThrGlnSerAspGlySerGlySerArgSerLeuGlyLeuAsnIleGly 152
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Db 236 GAATCTCCAAACAACTCATCATCAATGCAATTAAGGCTGTCGATCGAAAAAGGT 295
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Oy 153 GlyMetGlyAspTyrArgAsnGluThrLeu-----ThrThrAsnProArgAspThr 169
    |||||
Db 296 CATGGGCTGACGAACCTGATGAGTGTGTGGAGCCATGCACAAACCCGCGAGATCG 355
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Oy 170 AlaIleLeuSerHisLeuValGlnThrValPhePheLeuArg---GlyIleAspValVal 188
    |||||
Db 356 ACT-----AATGCACATTTTTCCTCCCTTACGGCGTAAAGCCATG 400
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Oy 189 SerProAlaAsnAlaAspThrAsp-----ValPhe 198
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Db 401 GCTCTCTGTAAGTAAACGTTTCAAGCCTCGAAGCTTCAAAATGCTCAATACGTGAG 460
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REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
199	leleam	-----lleaspaVal phegylThrIleargAanArgThclumechis	214	
461	CTGAACAAAGAGACTCTACTCTGAATCCCTTGATGATTAAGAAACGACGAGGTAACT	520		
215	leuTryaenAlaIuThrleuAlaIaGlnThrlyLeuGluTyPheAlaValaIaParg	234		
521	CTGCTGCAGCATCAAAATTTATCAACATCAGATAGAGACTTACTAC-----	565		
225	ThraAnlyLyLeuLeuIlelylePro-----LyethraenAla	247		
566	---AACCAAAAAGCTCTGCTGCCGACCTCTGGAACCTCGGTGACCTGTCATGGCAAAAGTG	622		
248	PhegiuaIaAlaTylyleGluAnserTy-----AlaLeuTyrMetGlyProTy	263		
623	TTTGGAACACTTAAGAGCTAAACCCCGGTAACTCGGCGCAGGTGGAGACTTAC	682		
264	LySValserTySGlyIlelylePro	271		
683	AAATCATCAAAAGTGTCTCAACT	706		
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CA192949		553 bp	mRNA	linear
LOCUS	SCRLSB1044F07.9	SBI Saccharum officinarum	CDNA clone	SCRLSB1044F07
DEFINITION	5', mRNA sequence.			
ACCESSION	CA192949			
VERSION	CA192949.1	GI:35139652		
KEYWORDS	EST.			
SOURCE	Saccharum officinarum			
ORGANISM	Saccharum officinarum			
REFERENCE	1 (bases 1 to 553)			
AUTHORS	Vector,A.L., da Silva,F.R., Kemper,E.L. and Arruda,P.			
TITLE	The libraries that made SUEST			
JOURNAL	Genet. Mol. Biol. 24 (1-4), 1-7 (2001)			
COMMENT	Contact: Arruda P Centro de Biologia Molecular e Engenharia Genetica Universidade Estadual de Campinas Caixa Postal 6010, 13083-970, Campinas SP, Brazil Tel: 55 19 3788 1137 Fax: 55 19 3788 1089 Email: patricia@unicamp.br Clome distribution information can be found through the Brazilian Clome Collection Center (BCCC) at http://www.bcccenter.fcav.unesp.br Plate: 044 row: F column: 07 Seq primer: T7 Promoter/Qualifiers Location/Qualifiers 1..553 /organism="Saccharum officinarum" /mol_type="mRNA" /db_xref="taxon:4547" /clone="SCRLSB1044F07" /lab_host="DH10B" /clone_1lb="SBI" /note="Organ: Stalk Bark from adult plants; Vector: pSport1, Site_1: SalI, Site_2: NotI; An unidirectional CDNA library generated from [Stalk Bark from adult plants] cDNA was prepared from polyA+ mRNA using Superscript Plasmid System Kit (Invitrogen). The double-strand cDNAs were fractionated in a sepharose cl-2B 40cm-column and fragments sizing between 0.8 and 1.5 Kb were directionally cloned into the vector. Details of each source of RNA and library construction can be obtained at http://eucest.fad.ic.unicamp.br/public"			

[illegible]

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/mol_type="genomic DNA"
/strain="Friedlin"
/db_xref="taxon:5664"
/clone="LB01/88a"
/lab_host="E. coli GeneHogs + TrfA"
/clone_1db="Leishmania major Friedlin BAC library"
/clone_2db="Leishmania major Friedlin in agarose blocks was partially
digested with HindIII, size selected, and ligated with
HindIII-digested pCG270 vector DNA. 10368 clones were
picked and arrayed in 384- and 96-well plates. Library
construction and arraying was carried out by ResGen
Corporation and clones and filters are available from
them"
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ORIGIN

Alignment Scores:

Pred. No.:	3.16	Length:	568
Score:	94.50	Matches:	38
Percent Similarity:	37.50%	Conservative:	13
Best Local Similarity:	27.94%	Mismatches:	38
Query Match:	5.74%	Indels:	47
DB:	8	Gaps:	6

US-10-617-835-4 (1-320) x BH87997 (1-568)

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QY 27 SerHisGlyGlyGlyArgPheAlaValGlnGlnLeuValAlaAlaSerAlaArg 46
   ::|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 154 GCTCAGGCGCGGTGCGCCGTTGTCGACAGAGAGGACCTATTGCTCAACGCG 213
   47 AlaAlaValIysAspMetAspLeuGlnAlaLeuHisGlyArgIysValAlaLeuTyrIle 66
   214 CAC-----CACGCGCGC-----CACGCGCGC-----CACGCGCGC----- 225
QY 67 AlaThrMetGlyAspGln-----CACGCGCGC-----CACGCGCGC----- 72
   ||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 226 ---ACCTTTCAGAGCAGTCGCGATGCGTCGCGCGCAACGTGCGGCTGTTGCCGT 282
   73 GlySerGlySerLeuThrGlyGlyArgTyrSerIleAspAlaLeuIleArgGlyIuTyr 92
   283 GGTGTCAGAGCAGTCGTTGGTGGCGCCACCGCTGACTGCTTG----- 327
QY 93 IleAsnSerProAlaValArgThrAspTyrThrTyrProArgTyrGluThrThrAlaGlu 112
   ||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 328 -----CCGAGCTCGCGCGCC-----GTTACAACTTTGGAG 357
QY 113 ThrThrSerGlyGlyLeuThrGlyLeuThrThrSerLeuSerThrLeuAsnAlaProAla 132
   ::|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 358 GCGGCGACAGGGGCGGCGTGGCAAACTATCCCGACAGCAGCACC--ACATGCAGTGCG 414
QY 133 LeuSerArgThrGlnSerAspGlySerGlySerArgSerSerLeuGly 148
   |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 415 TCCTTCGCGACCGCAGCTGCGAATGTTGGCATCTTGAAGCTGCTTGGC 462
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Search completed: August 18, 2005, 23:49:11
Job time : 3136 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame_plus.p2n model

Run on: August 19, 2005, 01:04:16 ; Search time 3941 Seconds
(without alignment)
3934.450 Million cell updates/sec

Title: US-10-617-835-4
Sequence: 1 MRARLLPILPSVFLSACG.....SHEGYGSDAVRHRGCGP 320

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Xgapop 60.0 , Xgapext 60.0
Ygapop 60.0 , Ygapext 60.0
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4708233 seqs, 24227607955 residues

Word size: 1

Total number of hits satisfying chosen parameters: 9408497

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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-LOOPT=0 -UNITS=bits -START=1 -END=1 -MATRIX=oligo -TRANS=human40.cdi
-LIST=45 -DOCALLIGN=200 -THR SCORE=quality -THR MIT=1 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pcio -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
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-NO MAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6
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Database :

GenEmbl:.*
1: gb_ba:.*
2: gb_hcg:.*
3: gb_in:.*
4: gb_cm:.*
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8: gb_pl:.*
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10: gb_ro:.*
11: gb_scs:.*
12: gb_sy:.*
13: gb_un:.*
14: gb_vl:.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	320	100.0	1136	6	A61825 Sequence 5
2	320	100.0	1136	6	AR393746 Sequence 1
3	320	100.0	3287	6	A61821 Sequence 1
4	320	100.0	3287	6	AR393745 Sequence 1

5	320	100.0	3294	1	AF142582	Neisseria
6	282	88.1	963	6	A96050	Sequence 83
7	282	88.1	963	6	AX043997	Sequence 83
8	207	64.7	963	6	A96046	Sequence 79
9	207	64.7	963	6	AX043995	Sequence 79
10	194	60.6	10869	1	AE002559	Neisseria
11	194	60.6	172325	6	AX044035	Sequence 81
12	179	55.9	963	6	A96048	Sequence 81
13	179	55.9	963	6	AX043999	Sequence 81
14	179	55.9	340806	1	NMA122491	Neisseria
15	179	55.9	640	6	A96044	Sequence 77
16	21	6.6	942	6	A96280	Sequence 31
17	21	6.6	942	6	A96282	Sequence 31
18	21	6.6	942	6	A96284	Sequence 31
19	21	6.6	10057	1	AE002420	Neisseria
20	21	6.6	11700	1	AE002393	Neisseria
21	21	6.6	195767	1	NMA722491	Neisseria
22	21	6.6	349980	6	AX044029	Sequence 31
23	21	6.6	349980	6	AX044030	Sequence 31
24	17	5.3	591	6	A96278	Sequence 31
25	10	3.1	156705	2	AC027270	Homo sapi
26	10	3.1	166236	2	AC022832	Homo sapi
27	10	3.1	167849	2	AC017001	Homo sapi
28	10	3.1	170517	2	AC069526	Homo sapi
29	10	3.1	175121	2	AC069246	Homo sapi
30	10	3.1	176017	2	AP002748	Homo sapi
31	10	3.1	182717	2	AC079823	Homo sapi
32	10	3.1	193264	2	AC090885	Homo sapi
33	10	3.1	198597	2	AC026218	Homo sapi
34	10	3.1	202844	9	AC090956	Homo sapi
35	10	3.1	229408	9	AC069271	Homo sapi
36	10	3.1	231972	2	AC068055	Homo sapi
37	9	2.8	663	8	AK107113	Oryza sat
38	9	2.8	758	6	BD145166	Primer fo
39	9	2.8	758	6	AX865104	Sequence
40	9	2.8	919	8	SLY011914	Solanum l
41	9	2.8	2339	5	BC067995	Xenopus t
42	9	2.8	10638	1	AE012364	Xanthomon
43	9	2.8	12705	1	AX345051	Sequence
44	9	2.8	12701	2	AC013927	Drosophila
45	9	2.8	16720	6	AX251815	Sequence

ALIGNMENTS

RESULT 1	A61825	1136 bp	DNA	linear	PAT 09-MAR-1998
LOCUS	A61825	Sequence 5 from Patent WO9711181.			
DEFINITION	A61825				
ACCESSION	A61825.1	GI:3715996			
VERSION					
KEYWORDS					
SOURCE	Neisseria gonorrhoeae				
ORGANISM	Neisseria gonorrhoeae				
REFERENCE	1	Meyer, T.F., Rudel, T., Scheuerpflug, I., Fischer, Eckhard and			
AUTHORS	Maler, J.				
TITLE	NUCLEIC ACID MOLECULES WHICH CODE PROTEINS WHICH MEDIATE THE				
JOURNAL	ADHESION OF NEISSERIA CELLS TO HUMAN CELLS				
COMMENT	PATENT: WO 9711181-A 5 27-MAR-1997;				
FEATURES	MAX PLANCK GEBELTSCHAFT (DE)				
source	Other Publication DE 19534579 970320.				
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	/organism="Neisseria gonorrhoeae"				
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 Query Match: 100.00% Indels: 0
 DB: 6 Gaps: 0

US-10-617-835-4 (1-320) x AR61825 (1-1136)

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Oy 1 MetatgAlaargleuileuileProilleuPheSerValPheilleuSerAlaCyegly 20
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Oy 21 ThrleuThrglyileProSerHiegllygllylsarPheAlaValgIngInleu 40
Db 195 ACACtGACAGGATTCATCCGATGCGGAGGCAACCTTCGCGGTGGAACAGAACTT 254
Oy 41 ValAlaAlaSerAlaargAlaAlaVallysaPheMetAspleuGlnAlaUhiaglYArg 60
Db 255 GTGGCCGCTTCTGCAGAGCTGCCGTTAAAGCATGATTTACAGCATTTACAGCAGCA 314
Oy 61 LysValAlaAleuYrilleAlaThrMetGlysaPngInglySerGlySerleuThrgly 80
Db 315 AAAGTTGATGTGATTCATTGCAACTATGGCGCACCAAGGTTCAAGCATTTGACAGGGG 374
Oy 81 ArgTySerIleasPAlaUhi1eArglygllyYrileasSerProAlaValArgThr 100
Db 375 CGCTACTCATTTGATGACTGATTCGCGGCAATTCATTAACAGCCCTCGCGCACCC 434
Oy 101 AspTyThrTyProArgTyrgluThrAlaGluThrThrseryglYleuThrgly 120
Db 435 GATTACACCTATCCGCTTACGAAACCAACCGCTGAAACATCAAGCGGTTTGAAGCGG 494
Oy 121 LeuThrThrserySerleuSerThrleuAsnAlaProAlaUhiSerArgThrgInSerAsp 140
Db 495 TTACACCACTTCTTTATCTAACACTTAATGCCCTGCACTCGCGCACCAATCAAGACG 554
Oy 141 SerGlySerIleasPAlaUhi1eArglygllyYrileasSerProAlaValArgThr 160
Db 555 AGCGGAAGTACAGAGCTGCTGGCTTAATATTCGCGGATGCGGGAATTCGAAATGA 614
Oy 161 ThrleuThrThrasPProArgAspThrAlaPheleuSerHiegllylsarPhe 180
Db 615 ACCTTGACGACCAACCCCGGACACTCTCTTCTTCCCACTGGTACAGACGCTATTT 674
Oy 181 PheleuAspGlyIleasPValIleSerProAlaAsnAlaAspThrasPValPheIleas 200
Db 675 TTCCGCGCGCATAGACGTTGTTCTCCGCAATGCGAATACAGATGTTTATTAC 734
Oy 201 IleasPValPheglYThrIleargAsnArgThrgIuMeChisLeuTyAsnAlaGluThr 220
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Oy 241 IleYsPProlystrAsnAlaPheGluAlaIleTyrlYsgluAsnTyAlaUhi1eUTrMet 260
Db 855 ATCAAAACCAAAACCAATGCGTTGAGCTGCTATTAAGAAATTAAGCAATGTGGATG 914
Oy 261 GlyProTyrlYsValserlysglyIleYsPProThrgInglyleuMetValAspPheSer 280
Db 915 GGGCGGATTAAGTAAGTAAGTAAGTAAGTAAGTAAGTAAGTAAGTAAGTAAGTAAGTA 974
Oy 281 AspIleargProTyrglyAsnHieThrglyAsnSerAlaProSerValGluAlaAspAsn 300
Db 975 GATATCCGCGCATACGCGAATCATACGCGTAATCTCCGCCCATCGTGAAGCGTATAC 1034
Oy 301 SerHieglInglyYrileasPProAlaValArgGlnHieArgGlnGlyPro 320
Db 1035 AGTCATGAGGGGATGATACAGCGATGACAGATGACAGCAACATTAAGAGGCAACT 1094
  
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RESULT 2
 AR393746 LOCUS 1136 bp DNA linear PAT 18-DEC-2003
 DEFINITION Sequence 6 from patent US 6617128.
 ACCESSION AR393746
 VERSION AR393746.1 GI:40120650
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 1136)
 AUTHORS Meyer,T.F., Rudel,T., Scheuenerflug,I., Maier,J., Eickernjager,S.,
 Schwan,T. and Fischer,B.
 TITLE Nucleic acid molecules encoding proteins which impart the adhesion
 of neisseria cells to human cells
 JOURNAL Patent: US 6617128-A 6 09-SEP-2003;
 FEATURES Location/Qualifiers
 source 1..1136
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 /mol_type="genomic DNA"

ORIGIN

Alignment Scores:
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 Best Local Similarity: 100.00% Mismatches: 0
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 DB: 6 Gaps: 0

US-10-617-835-4 (1-320) x AR393746 (1-1136)

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Db 195 ACACtGACAGGATTCATCCGATGCGGAGGCAACGCTTCGCGGTGGAACAGAACTT 254
Oy 41 ValAlaAlaSerAlaargAlaAlaVallysaPheMetAspleuGlnAlaUhiaglYArg 60
Db 255 GTGGCCGCTTCTGCAGAGCTGCCGTTAAAGCATGATTTACAGCATTTACAGCAGCA 314
Oy 61 LysValAlaAleuYrilleAlaThrMetGlysaPngInglySerGlySerleuThrgly 80
Db 315 AAAGTTGATGTGATTCATTGCAACTATGGCGCACCAAGGTTCAAGCATTTGACAGGGG 374
Oy 81 ArgTySerIleasPAlaUhi1eArglygllyYrileasSerProAlaValArgThr 100
Db 375 CGCTACTCATTTGATGACTGATTCGCGGCAATTCATTAACAGCCCTCGCGCACCC 434
Oy 101 AspTyThrTyProArgTyrgluThrAlaGluThrThrseryglYleuThrgly 120
Db 435 GATTACACCTATTCATTCATTCATTAATGCCCTGCACTCTCGGCAACCAATGACAGGT 554
Oy 121 LeuThrThrserySerleuSerThrleuAsnAlaProAlaUhiSerArgThrgInSerAsp 140
Db 495 TTACACCACTTCTTTATCTAACACTTAATGCCCTGCACTCTCGGCAACCAATGACAGGT 554
Oy 141 SerGlySerIleasPAlaUhi1eArglygllyYrileasSerProAlaValArgThr 160
Db 555 AGCGGAAGTACAGAGCTGCTGGCTTAATATTCGCGGATGCGGGAATTCGAAATGA 614
Oy 161 ThrleuThrThrasPProArgAspThrAlaPheleuSerHiegllylsarPhe 180
Db 615 ACCTTGACGACCAACCCCGGACACTCTCTTCTTCCCACTGGTACAGACGCTATTT 674
Oy 181 PheleuAspGlyIleasPValIleSerProAlaAsnAlaAspThrasPValPheIleas 200
Db 675 TTCCGCGCGCATAGACGTTGTTCTCCGCAATGCGAATGCAATGATGTTATTAC 734
Oy 201 IleasPValPheglYThrIleargAsnArgThrgIuMeChisLeuTyAsnAlaGluThr 220
  
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Db      735 ATCGAGCTATTTCGAAACGATACGCAACAGAACCGAAATCACCCTATACATGCCCCGAAACA 794
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Db      795 CTGAAGCCCAACAAACAACTGGAATATTTCGCGAGTGAAGACAAACCAATTAATAATGCTC 854
Qy      241 IleLVaSProLVaThrAsn1a1aPheG1ua1a1aTYrLVaG1uAseTYr1a1eUtrPheC 260
Db      855 ATCAAAACCAAAACCAATCGTTTGAAGCTGCTTAATAAGAAATTTACCATGTCGAGAG 914
Qy      261 G1yProTYrLVaSeSerLeuG1y11eLVaProThrg1uG1yLeuMeLVa1aSPheSer 280
Db      915 GGGCGGCTTAATAAGTAAGCAAGAAATCAACCGACGAGATTAATGCTCATTTCTCC 974
Qy      281 App11eagProTYrG1yVaSn1a1aThrg1yVaSnSer1a1aProSeVa1G1ua1aSPaen 300
Db      975 GATATCCGGCCATACGGCAATCATACGGGTAATCTCGCCCATCCGTAGAGGCTGATAAC 1034
Qy      301 Ser11eG1uG1yTYrG1yTYrSerAepG1ua1aVa1aArg1n1a1aArg1nG1yG1nPro 320
Db      1035 AGTCATGAGGGGTATGATACAGCATGAGCAAGTCGCAACATAGACAAAGGCAACT 1094

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RESULT 3
LOCUS      A61821                      3287 bp    DNA          linear    PAT 09-MAR-1998
DEFINITION Sequence 1 from Patent WO9711181.
ACCESSION  A61821
VERSION     A61821.1 GI:3715995
KEYWORDS
SOURCE
ORGANISM   Neisseria gonorrhoeae
            Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
            Neisseriaceae; Neisseria.
REFERENCE  1
            Meyer,T.F., Rudel,T., Scheuenerflug,I., Fischer, Eckhard and
            Maier,J.
            NUCLEIC ACID MOLECULES WHICH CODE PROTEINS WHICH MEDIATE THE
            ADHESION OF NEISSERIA CELLS TO HUMAN CELLS
            Patent: WO 9711181-A 1 27-MAR-1997;
            MAX PLANCK GEBELDSCHAFT (DE)
            Other publication DE 19534579 970320.
COMMENT
FEATURES
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                /mol_type="unassigned DNA"
                /strain="MS11"
                /db_xref="taxon:485"
                /clone_lib="GENOMISCHE BIBLIOTHEK IN PBA"

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ORIGIN
Alignment Scores:
Pred. No.:      0          Length:      3287
Score:          320.00      Matches:      320
Percent Similarity: 100.00%  Conservative: 0
Best Local Similarity: 100.00%  Mismatches: 0
Query Match:     100.00%      Indels:      0
DB:              Gaps:        0
US-10-617-835-4 (1-320) x A61821 (1-3287)

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Qy      1 MetAArg1a1aArgLeuLeu1ePro11eLeuPheSerVa1Phe11eLeuSer1a1aCYG1y 20
Db      583 ATGCGGCGCGGCTGTGATACCTATTCTTTTCGTTTATTTATTCAGCCCTGCGGG 642
Qy      21 ThrLeuThrg1y11eProSer11eG1yG1yLVaSPhe1a1aVa1G1uG1nG1uLeu 40
Db      643 AACACGACAGATTCATCGCATGCGGAGCGAAACGCTTGCGGTGAAACAAGACTT 702
Qy      41 Val1a1a1aSer1a1aArg1a1aVal1a1aSPeMetAepLeuG1n1a1eUhi1eG1yArg 60
Db      703 GTGGCGGCTTTCGCAAGACTGCGGTAAAGACATGAGATTTCAGGCAATTACACGACGA 762

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Qy      61 LVeVa1a1eLeuTYr11eAlaThrMeG1VaSPng1SeSerLeuThrg1yG1 80
Db      763 AAAGTTGCAATGTGATATTGCAACTATAGGCGGACCAAGGTTTCAGGAGTTTGACAGGGGT 822
Qy      81 ArgTYSer11eASp1a1eU11eArg1yG1uTYr11eAenSerPro1a1aVa1aArgThr 100
Db      823 CGCTACCTCATTTGATGACCTGATTGCGGCGGAATCATTAACAGCCCTGCGGTCGCAAC 882
Qy      101 AppTYrThrg1yProArgTYrG1uThrThra1aG1uThrThrSeG1yLVaThrg1y 120
Db      883 GATTACACCTTATCCCGCTTACGAAACCAACCGGTGAACAAATCATGAGCGGTTTGAAGG 942
Qy      121 LeuThrTrSerLeuSeThrLeuAen1a1aPro1a1eUSeSerArgThrg1nSeSerPgly 140
Db      943 TTAACTACCTTCTTATCTACACTTAATGCCCTGACACTCGCGCAATCCCAATCAGACGT 1002
Qy      141 SerG1ySeAr1gSeSerLeuG1yLeuAen11eG1yG1yMeG1yASeTYrArgAng1u 160
Db      1003 AGCGGAGTAAAGAGCAGTCTGGGCTTAATATTTGGCGGAGTGGGGAATTATCGAAATGA 1062
Qy      161 ThrLeuThrThraSPeThrg1aSPheThra1aPheLeuSer11eLeuVa1G1nThrVa1Phe 180
Db      1063 ACCTTGACGACCAACCCCGGACACCTGCTTTCTTCCACTTGCTACAGACCGTATTT 1122
Qy      181 PheLeuAArgG1y11eASpVa1a1aSePro1a1aAen1a1aSPThraSPVa1Phe11eAen 200
Db      1123 TTCTCGCGCGGCTATGACGTTGTTCTCTCTGCAATGCCGATACAGATGTTTATTAAAC 1182
Qy      201 11eASpVa1a1aPheG1yThr11eArgAen1a1aThrg1uMeTh1a1eUtyrAen1a1aG1uThr 220
Db      1183 ATCGAGTATTCCGAACCATACGCAACGAACCGAAATGCACTTATCAATGCGGAACA 1242
Qy      221 LeuLVa1a1eG1nThrLVaLeuG1uTYrPhe1a1aVa1a1aPArgThraSn1yLVaLeuLeu 240
Db      1243 CTGAAGCCCAACAAACCTGAATATTTCCACATGACAGAAACCAATTAATAATTTGCTC 1302
Qy      241 11eLVaSProLVaThraSn1a1aPheG1ua1a1aTYrLVaG1uAseTYr1a1eUtrPheC 260
Db      1303 ATCAAAACCAAAACCAATGCGTTGAAGCTGCTTAATAAGAAATTAAGCATTTGCGATG 1362
Qy      261 G1yProTYrLVaSeSerLeuG1y11eLVaProThrg1uG1yLeuMeLVa1aSPheSer 280
Db      1363 GGGCGGCTTAATAAGTAAGCAAGAAATCAACCGACGAGAAATTAATGTCGATTTCTCC 1422
Qy      281 App11eagProTYrG1yVaSn1a1aThrg1yVaSnSer1a1aProSeVa1G1ua1aSPaen 300
Db      1423 GATATCCGGCCATACGGCAATCATACGGGTAATCTCGCCCATCCGTAGAGGCTGATAAC 1482
Qy      301 Ser11eG1uG1yTYrG1yTYrSerAepG1ua1aVa1aArg1n1a1aArg1nG1yG1nPro 320
Db      1483 AGTCATGAGGGGTATGATACAGCATGAGCAAGTCGCAACATAGACAAAGGCAACT 1542

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RESULT 4
LOCUS      AR393745                      3287 bp    DNA          linear    PAT 18-DEC-2003
DEFINITION Sequence 1 from patent US 6617128.
ACCESSION  AR393745
VERSION     AR393745.1 GI:40120648
KEYWORDS
SOURCE
ORGANISM   Unknown.
            Uncloned.
REFERENCE  1 (bases 1 to 3287)
            Meyer,T.F., Rudel,T., Scheuenerflug,I., Maier,J., Bickernjager,S.,
            Schwan,T. and Fischer,E.
            Nucleic acid molecules encoding proteins which impart the adhesion
            of neisseria cells to human cells
            Patent: US 6617128-A 1 09-SEP-2003;
            Location/Qualifiers
                1..3287
                /organism="unknown"
                /mol_type="genomic DNA"
ORIGIN

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Alignment Scores:

Pred. No.:	0	Length:	3287
Score:	320.00	Matches:	320
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	6	Gaps:	0

US-10-617-835-4 (1-320) x AK393745 (1-3287)

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Qy      1 MetArgAlaArgLeuLeuIleProIleLeuPheSerValPheIleLeuSerAlaCysGly 20
Db      583 ATGGCGGACGCGCTGCTGATACCTATCTTTTTCGTTTATTTATTTATTCGCGCCGCGG 642
Qy      21 ThrLeuThrGlyIleProSerHisGlyGlyGlyAspPheAlaValGlnGlnLeu 40
Db      643 ACACGACAGAGATATTCATCCGATGCGGAGCGCAACCTTCGCGCGTCAACAAGAACTT 702
Qy      41 ValAlaAlaSerAlaArgAlaAlaValIysAspMetAspLeuGlnAlaLeuHisGlyArg 60
Db      703 GTGGCCGCTTCTGCCAGAGCTGCCCTTAAAGACATGATTTACAGGCATTTACAGGACGA 762
Qy      61 LysValAlaLeuYrIleAlaThrMetGlyAspGlnGlySerGlySerLeuThrGlyGly 80
Db      763 AAAGTTGCAATTGTACATTGCAACTATGGGCGACCAAGGTTGACGCGCAGTTGACAGGGGGT 822
Qy      81 ArgGlySerIleAspAlaLeuIleArgGlyGlyIleuYrIleAsnSerProAlaValArgThr 100
Db      823 CGCTACTCATTGATGACACTGATTCGCGCAATACATTAACAGCTTCGCGCGCCGCGCACCC 882
Qy      101 AspYrThrYrProArgYrGlyIleThrAlaGluThrSerGlyGlyLeuThrGly 120
Db      883 GATTACACCTATCCGCGGTACGAACAACCGCTGAAACAATACAGCGGTTGACGGGGT 942
Qy      121 LeuThrThrSerLeuSerThrLeuAsnAlaProAlaLeuSerArgThrGlnSerAspGly 140
Db      943 TTAAACCACTTCTTATCTACACTTAATGCCCTCGCACTCTCGCGCACCCCAATCAGACCGGT 1002
Qy      141 SerGlySerArgSerSerLeuGlyLeuAsnIleGlyGlyMetGlyAspYrFArgAspGly 160
Db      1003 AGCGGAATGAGAGAGAGTCTGGGCTTAAATATGGCGGAGATGGGGATTATCGAATGAA 1062
Qy      161 ThrLeuThrThrAsnProArgAspThrAlaPheLeuSerHisLeuValGlnThrValPhe 180
Db      1063 ACCTTGAGACCAACCCGCGGACACCTGCTTCTTCCACTTGTACACACCGTATTT 1122
Qy      181 PheLeuArgGlyIleAspValValSerProAlaAsnAlaAspThrAspValPheIleAsn 200
Db      1123 TTCTCGCGCGCATAGACGTTGTTCTCTCCCAATGCCGATACAGATGCTTTATTTAAC 1182
Qy      201 IleAspValPheGlyThrIleArgAsnArgThrGlnMetHisLeuYrAsnAlaGlyThr 220
Db      1183 ATCGACGATTCGAGACGATACGCAACGAACCGAAATGCACCTATACATGCCGAAACA 1242
Qy      221 LeuLysAlaGlnThrIleLeuGlyIleYrPheAlaValAspArgThrAsnLysLeuLeu 240
Db      1243 CTGAAGAGCCAAACAAACTGGAATATTTCCAGTAGACAGAACCAATPAAAAAATTTGGTCC 1302
Qy      241 IleLysProLysThrAsnAlaPheGlnAlaIleYrLysGlyIleuYrAlaLeuThrMet 260
Db      1303 ATCAAAACCCAAACCAATGCTTTGAAAGCTCCCTATTAAGAAATTAAGCAATTTGTGATG 1362
Qy      261 GlyProYrLysValSerLysGlyIleLysProThrGlnGlyLeuMetValAspPheSer 280
Db      1363 GGGCGCGTAAAGTAAGCAAGCAATCAACCGACGAGAGATTAATGTCGATTTCTCC 1422
Qy      281 AspIleArgProYrGlyAsnHisThrGlyAsnSerAlaProSerValGlnAlaAspAsn 300
Db      1423 GATATCCGGCCATACGGCAATCATACGGGTAACTCCGCCCATCGTACGAGCGATTAAC 1482
Qy      301 SerHisGlyGlyYrGlyYrSerAspGlnAlaValArgGlnHisArgGlnGlyIlePro 320

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Db 1483 AGTCATGAGGGGTATGATGATACAGCGATGAGCAAGTGGACAGACATAGACAAGGCAACT 1542

RESULT 5	LOCUS	DEFINITION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	FEATURES
AF142582	AF142582	Neisseria gonorrhoeae maf gene cluster, complete sequence.	1 (bases 1 to 3294)	Neisseria gonorrhoeae	Neisseria gonorrhoeae	Neisseria gonorrhoeae	Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales; Neisseriaceae; Neisseria.	Eickert, J., Meyer, T. F., Fischer, E., Mäler, J., Manning, P. A., Rudel, T. G., Scheuerpflug, I., Schulz, E. and Schwen, E. T.	Submitted (13-APR-1999) Molekulare Biologie, MPI fuer Infektionsbiologie, Monbijoustr. 2, Berlin 10117, Germany	location/Qualifiers	<p>1..3294</p> <p>/organism="Neisseria gonorrhoeae"</p> <p>/mol_type="genomic DNA"</p> <p>/strain="MS11"</p> <p>/db_xref="taxon:485"</p> <p>143..457</p> <p>/gene="mafI"</p> <p>143..457</p> <p>/gene="mafI"</p> <p>/codon_start=1</p> <p>/transl_table=11</p> <p>/product="MafI"</p> <p>/protein_id="AD31037.1"</p> <p>/db_xref="GI:4838553"</p> <p>/translation="MRSPRLSRKQKLIELFVAGVTARTAAEPDSIVTDCYRRYDV LDKERSHFRINSHTRFAERKHINNGINFMNPAKXHLKRFDOIPEHPEPYLKECER R"</p> <p>590..1552</p> <p>/gene="mafA"</p> <p>590..1552</p> <p>/gene="mafA"</p> <p>/codon_start=1</p> <p>/transl_table=11</p> <p>/product="adhesin MafA"</p> <p>/protein_id="AD31038.1"</p> <p>/db_xref="GI:4838554"</p> <p>/translation="MRARLLIPILPSVFILASGTLNGIPSHGGKRFAYEDELVAAS ARAAKMDMDQALHGKVALYITMDQSGSLTGGRYSIDALIREYINSFVPRVDY TYPRVETTAFTSGGLGLTSLSTINAPALSRQSDGSGSRSLGINTGMDYRNE TLVTNPEDNAFLSHLVQYVFLRGIDVSPANDVFINIDVFGTIRNTEMLTYNA ETLKQTKLEYFAVDRTNKLLIKPKTNVFEAAKYENVALMGPYVNSKGIKPTGLIM VDSDSIRPYCNHNGNSAPSVEDADNSHEGYSDSAVVRHOCOP"</p> <p>1592..3121</p> <p>/gene="mafB"</p> <p>1592..3121</p> <p>/gene="mafB"</p> <p>/codon_start=1</p> <p>/transl_table=11</p> <p>/product="adhesin MafB"</p> <p>/protein_id="AD31039.1"</p> <p>/db_xref="GI:4838555"</p> <p>/translation="MNLPLOKFMMLFAAISLIQITPSHANGLDARLDDMOAKHYEP GGRVHLFGNARGVKNRVCANVQTFDAIVAPLPIPTHERGFGIIGYETHFSGHGE VHPFPNHDKSTSDPSGVDGFTYQLIRTSGLHPADGYDGGGYPBPOGAKD IYSYHLKGTSTKTKINTVPOAPSPDRMLKENAGASGFLSRADAEAGLIEWNDPKAD RARMDIRGIVGAVNPPLTGGFVGVAITPSAVSPYVAARLTLOGITHGKINS PEAQDLAASLIQDSAPAVKDGINSAQMDAHNITRATQALAVEAAGTAKGVV ELNPTKMDVWKNTEYKPKPAKPMQIVDGEVAGNKKPKPSIQGHSTHSDNNTLPAPY VKPDTSLSPSGTIIQDRIRWTSKSPTEKSLNGHFKAHGKEFGDITLEDYQKASDLIS KQNSDKILGQYTBHRVRVDINNIIYVLNPKTFKIKTWMKPMIGREYVDGEFVKDGM N"</p>

ORIGIN

Alignment Scores:

Pred. No.: 0 Length: 3294
 Score: 320.00 Matches: 320
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 1 Gaps: 0

US-10-617-835-4 (1-320) x AF142582 (1-3294)

QY 1 MetArgAlaArgLeuLeuLeuLeuPheSerValPheIleuSerAlaCysGly 20
 DB 590 ATGGCGGACGGCTGCTGATACCTATCTTTTGGTTTATTTATTCGCGCTGGGG 649
 QY 21 ThrLeuThrGlyIleProSerHisGlyGlyValArgPheAlaValGluGluLeu 40
 DB 650 ACACGACAGCGATTCATCGCATGCGAGCGAAGCAACGCTTCGCGTCCAGCAAGAACTT 709
 QY 41 ValAlaIaIaSerAlaArgAlaAlaValLyAspMetAspLeuGluAlaLeuHisGlyArg 60
 DB 710 GTGGCCGCTTCTCCAGAGCTCCGTTAAAGCATGGATTTCAGGCATTACAGGACGA 769
 QY 61 LysValAlaLeuTyrIleAlaThrMetGlyAspGlnGlySerGlySerLeuThrGlyGly 80
 DB 770 AAAGTTGATTGTACATTGCACTATGGCGCAAGGTTCAAGGCGATTGACAGGGGGT 829
 QY 81 ArgTyrSerIleAspAlaLeuIleArgGlyGlyTyrIleAsnSerProAlaValArgThr 100
 DB 830 CGCTACTCATTTGAAGCACTGATTCGCGCGAATCATTAACAGCCCTGCCCTCCGCAAC 889
 QY 101 AspTyrThrTyrProArgTyrGlyThrThrAlaGluThrThrSerGlyGlyLeuThrGly 120
 DB 890 GATTACACTATCCCGCTTACGAAACCAACCGCTGAAACATCAGCGGTTTGAAGGGT 949
 QY 121 LeuThrThrSerLeuSerThrLeuAsnAlaProAlaLeuSerArgThrGlnSerAspGly 140
 DB 950 TTAACCACTTCTTTATCTTACACTTAATGCCCTGCACTCGCGACCCCAATCAGACGGT 1009
 QY 141 SerGlySerArgSerSerLeuGlyLeuAsnIleGlyGlyMetGlyAspTyrArgAsnGlu 160
 DB 1010 AGCGAAGATGAGAGCATGCTGGGCTTAAATATTTGGCGGGATGCGGATTAATGAATGAA 1069
 QY 161 ThrLeuThrThrAspProArgAspThrAlaPheLeuSerHisLeuValGluThrValPhe 180
 DB 1070 ACCTTGACGACCAACCGCGCGACACTGCTTCTTCCACTTGATGACGCGGATTT 1129
 QY 181 PheLeuArgGlyIleAspValValSerProAlaAsnAlaAspThrAspValPheIleAsn 200
 DB 1130 TTCCGCGCGGCGATAGACGTTGTTCTCTGCCAATGCCGATACAGATGTGTTATTAAAC 1189
 QY 201 IleAspValPheGlyThrIleArgAsnArgThrGluMetHisLeuTyrAsnAlaGluThr 220
 DB 1190 ATCGACGATTCGGAACGATACGCAACAGAACCGAAATGACCTTATACATCCCAAAACA 1249
 QY 221 LeuLysAlaGluThrThyLeuGluTyrPheAlaValAspArgThrAsnLysLeuLeu 240
 DB 1250 CTGAAGACCCAAACAACTGSAATATTTGCGAGTGAAGAACCAATTAATAATTTGCTC 1309
 QY 241 IleLysProLysThrAsnAlaPheGluAlaIaIaTyrLysGluAsnTyrAlaLeuTyrPhe 260
 DB 1310 ATCAAAACCAAAACCAATGCGTTTGAAGCTGCTTAAGAAATTAAGCAATTTGAGATG 1369
 QY 261 GlyProTyrLysValSerLysGlyIleLysProThrGluGlyLeuMetValAspPheSer 280
 DB 1370 GGGCGGATTAAGTAAGCAAGAAATCAAAACGAGAAAGATTAATGATTCATTTCTCC 1429
 QY 281 AspIleArgProTyrGlyAsnHisThrGlyAsnSerAlaProSerValGluAlaAspAsn 300
 DB 1430 GATATCCCGGCATAGGCAATCATCGGTAATCTCCGCCCATCCGTAGAGGCTGATTAAC 1489
 QY 301 SerHisGluGlyTyrGlyTyrSerAspGluAlaValArgGlnHisArgGlnGlyInPro 320
 DB 1490 AGTCATAGAGGGGTATGATGATACGATGAAAGCATGCGCAACATTAAGCAAGGCAACCT 1549

RESULT 6

A96050 963 bp DNA linear PAT 07-SEP-2000
 LOCUS A96050 Sequence 83 from Patent WO924578.
 DEFINITION A96050
 ACCESSION A96050
 VERSION A96050.1 GI:6779917
 KEYWORDS

SOURCE unidentified
 ORGANISM unidentified
 REFERENCE 1
 AUTHORS Neisserial antigens
 TITLE Pizza, M., Scarlato, V., Rappuoli, R., Grandi, G. and Masignani, V.
 JOURNAL Patient: WO 92/4578-A 83 20-MAY-1999;
 PIZZA MARIAGRAZIA (IT); SCARLATO VINCENZO (IT); RAPPUOLI RINO (IT);
 CHIRON SPA (IT); GRANDI GUIDO (IT); MASIGNANI VEGA (IT)

FEATURES

source 1..963
 /organism="unidentified"
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ORIGIN

Alignment Scores:

Pred. No.: 3,428-290 Length: 963
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 Percent Similarity: 99.38% Conservative: 0
 Best Local Similarity: 99.38% Mismatches: 1
 Query Match: 88.12% Indels: 2
 DB: 6 Gaps: 0

US-10-617-835-4 (1-320) x A96050 (1-963)

QY 1 MetArgAlaArgLeuLeuLeuLeuPheSerValPheIleuSerAlaCysGly 20
 DB 1 ATGGCGGACGGCTGCTGATACCTATCTTTTTCAGTTTATTTATTCGCGCTGGGG 60
 QY 21 ThrLeuThrGlyIleProSerHisGlyGlyValArgPheAlaValGluGluLeu 40
 DB 61 ACACGACAGGATTCATTCGATGCGAGCGAAGCAACCTTCGCGTCCAGCAAGAACTT 120
 QY 41 ValAlaIaIaSerAlaArgAlaAlaValLyAspMetAspLeuGluAlaLeuHisGlyArg 60
 DB 121 GTGGCCGCTTCTCCAGAGCTCCGTTAAAGCATGGATTTCAGGCATTACAGGACGA 180
 QY 61 LysValAlaLeuTyrIleAlaThrMetGlyAspGlnGlySerGlySerLeuThrGlyGly 80
 DB 181 AAAGTTGATTGTACATTGCACTATGGCGCAAGGTTCAAGGCGATTGACAGGGGGT 240
 QY 81 ArgTyrSerIleAspAlaLeuIleArgGlyGlyTyrIleAsnSerProAlaValArgThr 100
 DB 241 CGCTACTCATTTGAAGCACTGATTCGCGCGAATCATTAACAGCCCTGCCCTCCGCAAC 300
 QY 101 AspTyrThrTyrProArgTyrGlyThrThrAlaGluThrThrSerGlyGlyLeuThrGly 120
 DB 301 GATTACACTATCCCGCTTACGAAACCAACCGCTGAAACATCAGCGGTTTGAAGGGT 360
 QY 121 LeuThrThrSerLeuSerThrLeuAsnAlaProAlaLeuSerArgThrGlnSerAspGly 140
 DB 361 TTAACCACTTCTTTATCTTACACTTAATGCCCTGCACTCGCGACCCCAATCAGACGGT 420
 QY 141 SerGlySerArgSerSerLeuGlyLeuAsnIleGlyGlyMetGlyAspTyrArgAsnGlu 160
 DB 421 AGCGAAGATGAGAGCATGCTGGCTTAAATATTTGGCGGGAATGAGGATTAATGAATGA 480
 QY 161 ThrLeuThrThrAspProArgAspThrAlaPheLeuSerHisLeuValGluThrValPhe 180
 DB 481 ACCTTGACGACCAACCGCGCGACACTGCTTCTTCCACTTGATGACGCGGATTT 540
 QY 181 PheLeuArgGlyIleAspValValSerProAlaAsnAlaAspThrAspValPheIleAsn 200
 DB 541 TTCCGCGCGGCGATAGACGTTGTTCTCTGCCAATGCCGATACAGATGTGTTATTAAAC 600

Oy 201 ILeaspValPhegLYThrIleArgAsnArgThrGluMetHisLeuTYrAsnAlaGluThr 220
 Db 601 ATCGACGRTTCGGAACGATACGCAACGAACCGAAATGCACTTATACATGCCGAACA 660
 Oy 221 LeuLYsAlaGlnThrLYsLeuGluTYrPheAlaValAspArgThrAsnLYsLeuLeu 240
 Db 661 CTGAAGCCCAACCAAACTGGATATTTCCGAGTAGACAGAACCAATATAAAATTTGCTC 720
 Oy 241 ILeysProLYsThrAsnAlaPheGluAlaAlaTYrLYsGluAsnTYrAlaLeuTYrMet 260
 Db 721 ATCAAAACCAAAACCAATGCGTTGAGCTGCTATAAGAAATATAGCAATTGGAGATG 780
 Oy 261 GLYProTYrLYsValSerLYsGlyIleLYsProThrGluGlyLeuMetValAspPheSer 280
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 Db 841 GATATCCA-ACCATACGGCAATCATACGGGTAACTCCGCCCATCCGTAGAGGCTGATTA 899
 Oy 300 nSerHisGluGlyTYrGlyTYrSerAspGluAlaValArgGlnHisArgGlnGlyInPr 320
 Db 900 CAGTCATGAGGGGTATGATACGCGATGAAGCAGTGCAACAATAGACAAGGGCAACC 959
 Oy 320 o 320
 Db 960 T 960
 RESULT 7
 AX043997 963 bp DNA linear PAT 24-NOV-2000
 LOCUS Sequence 76 from Patent WO0066791.
 ACCESSION AX043997 GI:11342888
 VERSION AX043997.1
 KEYWORDS
 ORGANISM
 Neisseria gonorrhoeae
 Neisseria gonorrhoeae
 Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
 Neisseriaceae; Neisseria.
 REFERENCE
 1 Piazza,M., Hickey,E., Peterson,J., Tettelin,H., Venter,J.C.,
 Masiugnani,V., Galeotti,C., Mora,M., Ratti,G., Scarcelli,M.,
 Scarlato,V., Rappuoli,R., Frazer,C.M. and Grandi,G.
 Neisseria genomic sequences and methods of their use
 Patent: WO 0066791-A 76 09-NOV-2000;
 CHIRON CORPORATION (US) ; THE INSTITUTE FOR GENOMIC RESEARCH (US)
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 1. .963
 location/Qualifiers
 /organism="Neisseria gonorrhoeae"
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 Score: 282.00 Matches: 319
 Percent Similarity: 99.38% Conservative: 0
 Best Local Similarity: 99.38% Mismatches: 1
 Query Match: 88.12% Indels: 2
 DB: 6 Gaps: 0
 US-10-617-835-4 (1-320) x AX043997 (1-963)
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 Db 1 ATGCGGGGACCGGCTGCTGATACCTATTTCTTTTTCAGTTTATTTTATCCGCCGCGGG 60
 Oy 21 ThrLeuThrGlyIleProSerHisGlyGlyLYsArgPheAlaValGluGlnGlyLeu 40
 Db 61 ACACGTGACAGGTATTTCCATTCGCATGGCCGAGGCAAAACCTTCGCGGTGAACAACTT 120
 Oy 41 ValAlaAlaSerAlaArgAlaAlaValLYsAspMetAspLeuGlnAlaLeuHisGlyArg 60

Db 121 GTGGCCGCTTCGCAAGAGCTGCCGTTAAACATGATTTACAGGCACTTACAGGACGA 180
 Oy 61 LysValAlaLeuTYrIleAlaThrMetGlyAspGlnGlySerGlySerLeuThrGlyGly 80
 Db 181 AAAGTTGATTTGATTCATTGCAACTATGAGGCCACCAAGGTTGAGCAGATTACAGGGGGT 240
 Oy 81 ArgTYrSerIleAspAlaLeuIleArgGlyGlyTYrIleAsnSerProAlaValArgThr 100
 Db 241 CGCTACTCATTTGATTCAGTATTCGCGGCAATACATTAACACGCCCTGCGTCCGACCC 300
 Oy 101 AspTYrThrTYrProArgTYrGluThrThrAlaGluThrThrSerGlyLYsLeuThrGly 120
 Db 301 GATTACACCTATCCGCGTTACGAACCAACCGCTGAACCAATCATGAGGCGTTTACCGGGT 360
 Oy 121 LeuThrThrSerLeuSerThrLeuAsnAlaProAlaLeuSerArgThrGlnSerAspGly 140
 Db 361 TTAAACCACTTCTTATATCTACACTTAATGCCCTTCACCTCTGCGCACCAATCCAGACGGT 420
 Oy 141 SerGlySerArgSerSerLeuGlyLeuAsnIleGlyGlyMetGlyAspTYrArgAsnGlu 160
 Db 421 AGCCGAAGTAGAGCAAGCTGGGCTTAAATTTGGCGGAGTGGGGGATTATCGAAATGAA 480
 Oy 161 ThrLeuThrThrAsnProArgAspThrAlaPheLeuSerHisLeuValGlnThrValPhe 180
 Db 481 ACCTTGACAGACCAACCGCGGCACTGCGCTTTCTTCCCACTTGTCAGACCGGTAATTT 540
 Oy 181 PheLeuArgGlyIleAspValValSerProAlaAsnAlaAspThrAspValPheIleAsn 200
 Db 541 TTCCTGGCGGCAATGACGTTGTTCTCTGCCAATGCCGATACAGATGTTTATTTAAC 600
 Oy 201 ILeaspValPheGlyThrIleArgAsnArgThrGluMetHisLeuTYrAsnAlaGluThr 220
 Db 601 ATCGACGRTTCGGAACGATACGCAACGAACCGAAATGCACTTATACATGCCGAACA 660
 Oy 221 LeuLYsAlaGlnThrLYsLeuGluTYrPheAlaValAspArgThrAsnLYsLeuLeu 240
 Db 661 CTGAAGCCCAACCAAACTGGATATTTCCGAGTAGACAGAACCAATATAAAATTTGCTC 720
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 Oy 261 GLYProTYrLYsValSerLYsGlyIleLYsProThrGluGlyLeuMetValAspPheSer 280
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 Db 841 GATATCCA-ACCATACGGCAATCATACGGGTAACTCCGCCCATCCGTAGAGGCTGATTA 899
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 Db 960 T 960
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 A96046 963 bp DNA linear PAT 07-SEP-2000
 LOCUS Sequence 79 from Patent WO9924578.
 ACCESSION A96046
 VERSION A96046.1 GI:6779915
 KEYWORDS
 ORGANISM
 unidentified
 unidentified
 unclassified.
 REFERENCE
 1 Piazza,M., Scarlato,V., Rappuoli,R., Grandi,G. and Masiugnani,V.
 TITLE Neisserial antigens
 JOURNAL Patent: WO 9924578-A 79 20-MAY-1999;

Qy	143	SerArg-SerSerLeuGlyLeuAenIleGlyIwMcGlyAspTyrArgAenIuThle	162
Db	427	AGTAA-ANGAGTCTGGCTTAATATTGGCGGATGGGGATTATCGAAATGAACCTT	485
Qy	162	uThrThsAsnProArgrAspThrAlaPheLeuSerHisLeuValGlnThrValPhePheLe	182
Db	486	GAGACATNACCCGGCGACATGCTCTTCTTCCCACTTGATACGACCGTATTTTCTCT	545
Qy	182	uArgGlyIleAspValValSerProAlaAsnAlaAspThrAspValPheIleAsnIleAs	202
Db	546	GCGGGGATAGACGTTGTTCTTCCTGCAATGCCATACAGATGTTATTATTAACATCGA	605
Qy	202	pValPheGlyThrIleArgAsnArgThrGluMethIstLeuTyrAsnAlaGluThrLeuLy	222
Db	606	CGTATTCGGAACGATACCCACAGAACCGAAATGCACTTATACAAATGCCGAACATCTAA	665
Qy	222	sAlaGlnThrIstLeuGlyIstLeuPheAlaValAspArgThrAsnIstLeuIleuIleLy	242
Db	666	AGCCCAACAAACCTGGAATATTTGCGAGTAGACGAAACCAATAAAAATGCTCATCAA	725
Qy	242	sProLyThrAsnAlaPheGluAlaAlaTyrLyGluAsnTyrAlaLeuTpmetGlyPr	262
Db	726	ACCAAAAAACCAATCGTTGAAGCTGCTATTAAGAAATTAACGATTTGATGAGGGGCC	785
Qy	262	oTyrLyValSerIstLeuGlyIstLeuProThrGluGlyLeuMetValAspPheSerAspI	282
Db	786	GTATTAAGTAAAGCAAGAAATTAAACGACGAAAGATTAATGTCATTTCTCCGATAT	845
Qy	282	eArgProTyrGlyAsnHisThrGlyAsnSerAlaProSerValGluAlaAspAsnSerHi	302
Db	846	CCGACCATACCGGCATCATACGGGTAACTCCGCCCATCCGTAGAGGCTGATAACATCA	905
Qy	302	sGluGlyTyrGlyTyrSerAspGlu	310
Db	906	TGAGGGGATGATACAGCGATGAA	930
RESULT 10			
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LOCUS	Neisseria meningitidis serogroup B strain MC58 section 201 of 206		
DEFINITION	Neisseria meningitidis serogroup B strain MC58 section 201 of 206		
ACCESSION	AE002559		
VERSION	AE002098		
KEYWORDS	AE002559.2 GI:7413482		
SOURCE	Neisseria meningitidis MC58		
ORGANISM	Neisseria meningitidis MC58		
REFERENCE	Neisseria meningitidis MC58		
AUTHORS	Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales; Neisseriaceae; Neisseria.		
	1 (bases 1 to 10869)		
	Tettelin,H., Saunders,N.J., Heidelberg,J., Jeffries,A.C., Nelson,K.E., Eisen,J.A., Ketchum,K.A., Hood,D.W., Peden,J.F., Dodson,R.J., Nelson,W.C., Gwinn,M.L., DeBoy,R., Peterson,J.D., Hickey,E.K., Haft,D.H., Salzberg,S.L., White,O., Fleischmann,R.D., Dougherty,B.A., Mason,T., Ciecko,A., Parksey,D.S., Blait,E., Clifton,H., Clark,E.B., Cotton,M.D., Uteirpack,T.R., Khouri,H., Qin,H., Vamathevan,J., Gill,J., Scarlato,V., Masiagnani,V., Piazza,M., Grandi,G., Sun,L., Smith,H.O., Fraser,C.M., Moxon,E.R., Rappuoli,R. and Venter,J.C.		
TITLE	Complete genome sequence of Neisseria meningitidis serogroup B strain MC58		
JOURNAL	Science 287 (5459), 1809-1815 (2000)		
MEDLINE	20175755		
PUBMED	10710307		
REFERENCE	2 (bases 1 to 10869)		
AUTHORS	Tettelin,H., Saunders,N.J., Heidelberg,J., Jeffries,A.C., Nelson,K.E., Eisen,J.A., Ketchum,K.A., Hood,D.W., Peden,J.F., Dodson,R.J., Nelson,W.C., Gwinn,M.L., DeBoy,R., Peterson,J.D., Hickey,E.K., Haft,D.H., Salzberg,S.L., White,O., Fleischmann,R.D., Dougherty,B.A., Mason,T., Ciecko,A., Parksey,D.S., Blait,E., Clifton,H., Clark,E.B., Cotton,M.D., Uteirpack,T.R., Khouri,H., Qin,H., Vamathevan,J., Gill,J., Scarlato,V., Masiagnani,V., Piazza,M., Grandi,G., Sun,L., Smith,H.O., Fraser,C.M., Moxon,E.R., Rappuoli,R. and Venter,J.C.		

TITLE	Direct Submission
JOURNAL	Submitted (17-MAR-2000) The Institute for Genomic Research, 9712 Medical Center Dr, Rockville, MD 20850, USA
COMMENT	On Apr 4, 2000 this sequence version replaced gi:7227357.
FEATURES	Location/Qualifiers
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CDS	150..524
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gene	complement (712..2178)
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CDS	complement (712..2178)
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gene complement (3366, .3947)
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YKGSADVARKIGIIVAAKPCVSEAEVDAETVEKERIYITQALASGKPDIAKMY
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identified by sequence similarity; putative"
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Alignment Scores:
Pred. No.: 2,1e-195 Length: 10869
Score: 194.00 Matches: 307
Percent Similarity: 99.03% Conservative: 0
Best Local Similarity: 99.03% Mismatches: 1
Query Match: 60.62% Indels: 3
DB: 1 Gaps: 0

US-10-617-835-4 (1-320) x AEO02559 (1-10869)

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DB 7268 GCAAGCGCTGCGATACCTATCTTTTCAGTTTATTTATCCGCTGCGGACACTG 7327
QY 23 ThrGlyIleProSerHicGlyGlyGlyIysaRghaIalaGluGlnGluLeuVala 42
DB 7328 ACAGGATTCATCGATCGAGCGAGTAACGCTTGGGTCGAAACAAGCTTGCGCC 7387
QY 43 AAlaSerAlaIaGlaIaIaValIleValMetSerLeuGlnIaLeuHicGlyIaRgIyVal 62
DB 7388 GCTTGTGCAAGCGCGCGGTAAAGACATGATTACAGGCAATTACACGGAAGAAAGT 7447
QY 63 AAlaLeuYrIleAlaThMetGlyIaSerGlnIySerGlySerLeuThrGlyIaRgTy 82
DB 7448 GCATTGTACATTCGACATGCGACCAAGGTTAGGCACTTACAGGGGGGCGCTA 7507
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DB 7568 CACCTATCCAGCTTACGAAACCAACCGCTGAACAACATCAGCGGTTGACAGGTTTAA 7627
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DB 7628 CACTTCTTATCTACATTAATGCCCCCTGCACTCTGCAACCAATCAGACGATAGCG 7687
QY 142 ySerArgSerSerLeuGlyLeuAaIleGlyIyMetGlyIaAaPtyrArgaengIuThr 162
DB 7688 AAGTAA-AAAGCAGTGTGGCTTAATATATGGCGGATGGGGATATATGAAATGAACCT 7746
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DB 7747 TGACGACTAACCCGCGACACTGCTTCTTCTCCACTGTGATACAGACCGATTTTTC 7806
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DB 7807 TGCGCGGATAGACGTTTCTCTCTGCAATGCCGATACAGATGTTTATTAATCATCG 7866
QY 202 spValPheGlyThrIleArgAaAaRgThrGluMetHicLeuTyrAaAlaGluThrLeu 222
DB 7867 ACGTATTCGGAACGATACGAAACGAAATGCACTATACAAATGCCGAACACTGA 7926

Qy 222 ysa1agiInThrlYsleuGluYrPhealValAspArgThrAsnYsYsleuLeuIel 242
Db 7927 AAGCCCAACAAATGGAAATATTTGCGATGACAGAACCAATATAAAATGGCATCA 7986
Qy 242 ySProlYsThrAsnAlaPheGluAlaAlaYrYsGluAsnYrAlaLeuTrpMetGlyP 262
Db 7987 AACCAAAACCAATGCGTTTGAAGCTGCGCTATAAAGAAAATTAGCATTTGGATGGGCG 8046
Qy 262 rOTYrYsValSerYsGlyIleYsP-OTThrGluGlyLeuMetValAspPheSerAspI 282
Db 8047 CGTATAAAGTAAGCAAAAGAAATTAACCGACGGAAGATTAATGCTCATTTCTCCGATA 8106
Qy 282 leaSPProTYrGlyAsnHisThrGlyAsnSerAlaProSerValGluAlaAspAsnSerH 302
Db 8107 TCCGACCATACGGCAATCATACGGGTAACTCGCCCATCCGTAGAGCTATTAACAATC 8166
Qy 302 isGluGlyTYrGlyTYrSerAspGlu 310
Db 8167 ATGAGGGGTATGATACAGCGATGAA 8192

RESULT 11
AX044035 172325 bp DNA linear PAT 24-NOV-2000
LOCUS Sequence 114 from Patent WO0066791.
DEFINITION AX044035
ACCESSION AX044035
VERSION AX044035.1 GI:11342919
KEYWORDS
SOURCE
ORGANISM
Neisseria meningitidis
Neisseria meningitidis
Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
Neisseriaceae; Neisseria.
REFERENCE
AUTHORS
1 Pizzo, M., Hickey, E., Peterson, J., Tettelin, H., Venter, J. C.,
Wasingham, V., Galeotti, C., Mora, M., Ratti, G., Scarlato, V.,
Scarlato, V., Rappuoli, R., Fraxer, C. M. and Grandi, G.
TITLE
Neisseria genomic sequences and methods of their use
JOURNAL
Patent: WO 0066791-A 114 09-NOV-2000;
CHIRON CORPORATION (US); THE INSTITUTE FOR GENOMIC RESEARCH (US)
FEATURES
SOURCE
location/Qualifiers
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ORIGIN
Alignment Scores:
Pred. No.: 2.83e-194 Length: 172325
Score: 194.00 Matches: 307
Percent Similarity: 99.03% Conservative: 0
Best Local Similarity: 99.03% Mismatches: 1
Query Match: 60.62% Indels: 3
DB: 6 Gaps: 0
US-10-617-835-4 (1-320) x AX044035 (1-172325)

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Qy 102 rThrTYrProArgGlyGluYrThrAlaGluYrThrSerGlyGlyLeuThrGlyLeuTh 122
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Qy 142 ySerArg-SerSerIleuGlyLeuAsnIleGlyGlyMetGlyAspTYrArgAsnGluThrl 162
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Qy 162 eUTHrThrAsnProArgAspThrAlaPheLeuSerHisLeuValGluThrValPhePheL 182
Db 122177 TGACGACATTAACCCCGGACACTGCCCTTTCTTCCACTTGGTACAGACCGTATTTTCC 122236
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Qy 262 rOTYrYsValSerYsGlyIleYsP-OTThrGluGlyLeuMetValAspPheSerAspI 282
Db 122477 CGTATAAAGTAAGCAAAAGAAATTAACCGACGGAAGATTAATGCTCATTTCTCCGATA 122536
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RESULT 12
A96048 963 bp DNA linear PAT 07-SEP-2000
LOCUS Sequence 81 from Patent WO924578.
DEFINITION A96048
ACCESSION A96048
VERSION A96048.1 GI:6779916
KEYWORDS
SOURCE
unidentified
unidentified
ORGANISM
unclassified.
REFERENCE
AUTHORS
1 Pizzo, M., Scarlato, V., Rappuoli, R., Grandi, G. and Wasingham, V.
TITLE
Neisserial antigens
JOURNAL
Patent: WO 924578-A 81 20-MAY-1999;
PIZZA MARIAGRAZIA (IT); SCARLATO VINCENZO (IT); RAPPUOLI RINO (IT);
CHIRON SPA (IT); GRANDI GUIDO (IT); MASIGNANI VEGA (IT)
FEATURES
SOURCE
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/organism="unidentified"

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ACCESSION	segment 1/7.
VERSION	AL162752 AL157959
KEYWORDS	ALI62752.2 GI:7378778
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ORGANISM	Neisseria meningitidis Z2491 Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales; Neisseriaceae; Neisseria.
REFERENCE	1 (bases 1 to 340806)
AUTHORS	Parkhill,J., Achtman,M., James,K.D., Bentley,S.D., Churcher,C., Klee,S.R., Morelli,G., Basham,D., Brown,D., Chillingworth,T., Davies,R.M., Davis,P., Devlin,K., Feltwell,T., Hamlin,N., Holroyd,S., Jagers,K., Leathe,S., Moulé,S., Mungall,K., Quail,M.A., Rajandream,M.A., Rutherford,K.W., Simmonds,M., Skelton,J., Whitehead,S., Spratt,B.G. and Barrell,B.G. Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491 Nature 404 (6777), 502-506 (2000) 22022556 MEDLINE PUBMED 10761919 2 (bases 1 to 340806) REFERENCE Parkhill,J. Direct Submission Submitted (30-MAR-2000) Submitted on behalf of the Neisseria sequencing team, Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA E-mail: parkhill@sanger.ac.uk JOURNAL
COMMENT	Notes: Details of N. meningitidis sequencing at the Sanger Centre are available on the World Wide Web. (URL, http://www.sanger.ac.uk/Projects/N_meningitidis/). Location/Qualifiers 1..340806 /organism="Neisseria meningitidis Z2491" /mol_type="genomic DNA" /strain="Z2491" /db_xref="taxon:122587" /note="serogroup: A" complement(38..358) /gene="NMA0001" complement(38..358) /gene="NMA0001" note="NMA0001, unknown, len: 106 aa" /codon_start=1 /transl_table=11 product="hypothetical protein NMA0001" /protein_id="CAB83321.1"
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putative mobilization protein (200 aa), fasta scores; E():
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US-10-617-835-4 (1-320) x NMA122491 (1-340806)

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DEFINITION Sequence 77 from Patent WO924578.
ACCESSION A96044
VERSION A96044.1 GI:6779914
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
unclassified.

REFERENCE 1
AUTHORS Pizsa, M., Scarlato, V., Rappuoli, R., Grandi, G. and Maignani, V.
TITLE Neisserial antigens
JOURNAL Patent: WO 9924578-A 77 20-MAY-1999;
PIZZA MARIAGRAZIA (IT); SCARLATO VINCENZO (IT); RAPPUOLI RINO (IT);
CHIRON SPA (IT); GRANDI GUIDO (IT); MALIGNANI VEGA (IT)
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FEATURES
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US-10-617-835-4 (1-320) x A96044 (1-640)

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GenCore version 5.1.6
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6	107.5	6.5	9025608	15 US-10-156-261-1	Sequence 1, Appl1
7	104.5	6.4	1163020	17 US-10-398-221-10	Sequence 2058, Ap
8	104.5	6.4	3011208	17 US-10-398-221-2058	Sequence 87537, A
9	103.5	6.3	2604	19 US-10-437-963-87357	Sequence 16487, A
10	101	6.1	1335	17 US-10-282-122A-16487	Sequence 12803, A
11	101	6.1	1795	18 US-10-425-114-12803	Sequence 56736, A
12	101	6.1	1946	18 US-10-424-589-56736	Sequence 118877, A
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16	98.5	6.0	939	17 US-10-241-742-69	Sequence 69, Appl1
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31	94.5	5.7	1089	14 US-10-206-576-157	Sequence 157, App
32	94.5	5.7	1089	21 US-10-912-362-157	Sequence 485, App
33	94.5	5.7	1929	9 US-09-070-927A-485	Sequence 8649, Ap
34	94.5	5.7	2025	18 US-10-425-114-6649	Sequence 110807, A
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36	94	5.7	1293	17 US-10-282-122A-17669	Sequence 14952, A
37	94	5.7	1461	19 US-10-437-963-14952	Sequence 1, Appl1
38	94	5.7	9025608	15 US-10-156-761-1	Sequence 5949, Ap
39	93.5	5.7	3000	15 US-10-156-761-5949	Sequence 14432, A
40	93.5	5.7	3222	17 US-10-282-122A-14432	Sequence 2, Appl1
41	93.5	5.7	3816	21 US-10-875-518-2	Sequence 12158, A
42	93	5.7	1038	17 US-10-437-963-12158	Sequence 15413, A
43	93	5.7	1356	17 US-10-282-122A-15413	Sequence 13676, A
44	93	5.7	1404	19 US-10-767-701-13676	Sequence 30610, A
45	93	5.7	2253	17 US-10-282-122A-30610	

ALIGNMENTS

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RESULT 1
US-09-043-302-6
; Sequence 6, Application US/09043302
; Publication No. US20020086349A1
;
GENERAL INFORMATION:
; APPLICANT: MEYER, Thomas F.
; APPLICANT: RUDEL, Thomas
; APPLICANT: SCHUEERPLUG, Ina
; APPLICANT: MAIER, Jurgen
; APPLICANT: EICKENJAGER, Sandra
; APPLICANT: SCHMIDT, Thomas
; TITLE OF INVENTION: Nucleic Acid Molecules Encoding Proteins Which Impart
; FILE REFERENCE: 0147-172P
; CURRENT APPLICATION NUMBER: US/09/043,302
; CURRENT FILING DATE: 1998-06-08
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Pred. No. is the number of results predicted by chance to have a

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; EARLIER APPLICATION NUMBER: PCT/EP96/04092
; EARLIER FILING DATE: 1995-09-18
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Patencin Ver. 2.0
; SEQ ID NO 6
; LENGTH: 1136
; TYPE: DNA
; ORGANISM: Neisseria gonorrhoeae
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (135)..(1094)
; US-09-043-302-6

Alignment Scores:
Pred. No.:      3,21e-193      Length:      1136
Score:          1645.00      Matches:      320
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match:      100.00%      Indels:      0
DB:               9          Gaps:      0

US-10-617-835-4 (1-320) x US-09-043-302-6 (1-1136)

Qy      1 MetArgAlaArgLeuLeuIleProIleLeuPheSerValPheIleLeuSerAlaCysGly 20
Db      135 ATGGCGGACGCGCTGCTGATACCTATCTTTTTCGTTTATTTATTCGCCCTGCGCGG 194

Qy      21 ThrLeuThrGlyIleProSerHisGlyGlyLysArgPheAlaValGlnGlnLeu 40
Db      195 ACACGACAGGATATTCATCGCATGGCGGAGCAAAACCTTCGCGGTGAAACAAACTT 254

Qy      41 ValAlaIaSerAlaArgAlaAlaValLysAspMetAspLeuGlnAlaLeuHisGlyArg 60
Db      255 GTGGCCGCTTTCGCGACGAGCTCCGCTTAAAGACATGATTTACAGCATTTACAGGACGA 314

Qy      61 LysValAlaLeuYrIleAlaThrMetGlyAspGlnGlySerGlySerLeuThrGly 80
Db      315 AAAGTTGCATTGTACATTCGCAACTATGGGCGACCAAGGTTTCAGGACAGTTCGACAGGGGT 374

Qy      81 ArgTyrSerIleAspAlaLeuIleArgGlyGlyUryrIleAsnSerProAlaValArgThr 100
Db      375 CGCTACCTCATTTGATGACATGATTCGCGCGCAATACATTAACAGCCCTGCGCACCC 434

Qy      101 AspTyrThrTyrProArgTyrGlyUthrThrAlaGlnThrThrSerGlyLeuThrGly 120
Db      435 GATTACACCTATCCGCGTTAGAAACCAACCGGTGAACAACATCAGGGGTTTGAAGGGT 494

Qy      121 LeuThrThrSerLeuSerThrLeuAsnAlaProAlaLeuSerArgThrGlnSerAspGly 140
Db      495 TTAAACCACTTCCTTATCTACACTTATATGCCCTGCACCTCGCGCACCAATCAACACGT 554

Qy      141 SerGlySerArgSerSerLeuGlyLeuAsnIleGlyGlyMetGlyAspTyrArgAsnGly 160
Db      555 AGCGGAATGAGAGAGAGCTGGGCTTAAATATTCGCGGAGATGGGAGATTATCGAAATGAA 614

Qy      161 ThrLeuThrThrAsnProArgAspThrAlaPheLeuSerHisLeuValGlnThrValPhe 180
Db      615 ACCTTGACGACCAACCCGCGGACACCTGCTTTTCCACTTGATGACAGCGGATTT 674

Qy      181 PheLeuAlaGlyIleLeuAspValValSerProAlaAsnAlaAspThrAspValPheIleAsn 200
Db      675 TTCCTGCGCGCATGAGAGTGTCTCTCGCAATGCGCATACGATGTGTTATTTAAC 734

Qy      201 IleAspValPheGlyThrIleArgAsnArgThrGlnMetHisLeuTyrAsnAlaGlnThr 220
Db      735 ATCGACGATTCGGAACCATACGCAACGAAACGAAATGCACCTTATCAATGCGGAAACA 794

Qy      221 LeuLysAlaGlnThrLysLeuGlnTyrPheAlaValAspArgThrAsnLysLeuLeu 240
Db      795 CTGAAAGCCCAAAACCTGGAATATTTTCGACATGACAGAACCAATAAAAAATTTGCTC 854

Qy      241 IleLysProLysThrAsnAlaPheGlnAlaAlaIleTyrLysGlnSerTyrAlaLeuTrpMet 260

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Db      855 ATCAAAACCAAAACCAATGCCTTTGAACTGCTTAATAAGAAAATTACGATTTGATG 914
Qy      261 GlyProTyrLysValSerLysGlyIleLysProThrGlnGlyLeuMetValAspPheSer 280
Db      915 GGGCCGTATAAGTAAGTAAGAAAGAAATCAACCGACGGAGGAATTAATGATTTCTCC 974

Qy      281 AspIleArgProTyrGlyAsnHisThrGlyAsnSerAlaProSerValGlnAlaAspAsn 300
Db      975 GATATCCGGCCATACGGGAATCATACGGGTAACTCCGCCCATCGGTAGAGGCTGATAC 1034

Qy      301 SerHisGlnGlyTyrGlyTyrSerAspGlnAlaValArgGlnHisArgGlnGlyGlnPro 320
Db      1035 AGTCATGAGGGGTATGATGATACAGGAGATGAAACAGTGCACAACTAGCAAGGGCAACT 1094

RESULT 2
US-10-617-835-6
; Sequence 6, Application US/10617835
; Publication No. US20050124037A1
; GENERAL INFORMATION:
; APPLICANT: MEYER, Thomas F.
; APPLICANT: RUDEL, Thomas
; APPLICANT: SCHUEBERPFLUG, Ina
; APPLICANT: MAIER, Jurgen
; APPLICANT: EICKENMUEGER, Sandra
; APPLICANT: SCHWAN, Thomas
; TITLE OF INVENTION: Nucleic Acid Molecules Encoding Proteins Which Impart
; FILE REFERENCE: 0147-172P
; CURRENT APPLICATION NUMBER: US/10/617, 835
; CURRENT FILING DATE: 2003-07-14
; PRIOR APPLICATION NUMBER: US/09/043,302
; PRIOR FILING DATE: 1998-06-08
; PRIOR APPLICATION NUMBER: PCT/EP96/04092
; PRIOR FILING DATE: 1995-09-18
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Patencin Ver. 2.0
; SEQ ID NO 6
; LENGTH: 1136
; TYPE: DNA
; ORGANISM: Neisseria gonorrhoeae
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (135)..(1094)
; US-10-617-835-6

Alignment Scores:
Pred. No.:      3,21e-193      Length:      1136
Score:          1645.00      Matches:      320
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match:      100.00%      Indels:      0
DB:               22          Gaps:      0

US-10-617-835-4 (1-320) x US-10-617-835-6 (1-1136)

Qy      1 MetArgAlaArgLeuLeuIleProIleLeuPheSerValPheIleLeuSerAlaCysGly 20
Db      135 ATGGCGGACGCGCTGCTGATACCTATCTTTTTCGTTTATTTATTCGCCCTGCGCGG 194

Qy      21 ThrLeuThrGlyIleProSerHisGlyGlyLysArgPheAlaValGlnGlnLeu 40
Db      195 ACACGACAGGATATTCATCGCATGGCGGAGCAAAACCTTCGCGGTGAAACAAACTT 254

Qy      41 ValAlaIaSerAlaArgAlaAlaValLysAspMetAspLeuGlnAlaLeuHisGlyArg 60
Db      255 GTGGCCGCTTTCGCGACGAGCTCCGCTTAAAGACATGATTTACAGCATTTACAGGACGA 314

Qy      61 LysValAlaLeuYrIleAlaThrMetGlyAspGlnGlySerGlySerLeuThrGlyGly 80
Db      315 AAAGTTGCATTGTACATTCGCAACTATGGGCGACCAAGGTTTCAGGACAGTTCGACAGGGGT 374

Qy      81 ArgTyrSerIleAspAlaLeuIleArgGlyGlyUryrIleAsnSerProAlaValArgThr 100

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Db      375 CGCTACTGATGATGACTGATTCGGGGGAATACATAACAGCCCTGCGCGACC 434
Qy      101 AapTYrThTYrProArqTYrGLuThrThraIaGIuThrThSergIyGLyLeuThrgIy 120
Db      435 GATTACACCTATCCGGGTACGAAACCAACCGCTGAAACAAACATCAAGCGGTGACGGGT 494
Qy      121 LeuThrThSergSerThrLeuAsnAlaProAlaLeuSerArqThrgIInserAspGly 140
Db      495 TTAAACCACTCTTTATCTACCTTAATAGCCCTGACCTCGCGCAACCCAAACAGACGGT 554
Qy      141 SerGIySerArqSerSerLeuGLyLeuAsnIleGIyGLyMetGIyAspTYrArqAnglu 160
Db      555 AGCGAAGTAGAGACGAGCTGGGCTTAATATTGGCGGATGGGGATTATGAAATGA 614
Qy      161 ThrLeuThrThAsnProArqAspThraIaPheLeuSerHisLeuValGIuThrValPhe 180
Db      615 ACCTTGACACCAACCCCGCGACACTGCTTCTTCCCACTGGTACAGACCGATATT 674
Qy      181 PheLeuArqGIyIleAspValIaSerProAlaAsnAlaAspThrAspValPheIleAsn 200
Db      675 TTCCTGGCGGAGATAGACGTGTGTTCTCCTGCCAATGCGATACAGATGTGTTATTAC 734
Qy      201 IleAspValPheGIyThrIleArqAsnArqThrgIuMetHisLeuTYrAsnIaGIuThr 220
Db      735 ATCGACGATTCGGAACGATACGCAACAGAACGAAATGCACCTATACAAATCCGAAACA 794
Qy      221 LeuLYsAlaGIuThrLYsLeuGLuTYrPheAlaValAspArqThrAsnLYsLYsLeuLeu 240
Db      795 CTGAAGACGCCAAACAAACATCGAATATTTCCGACGTAGACAGAACCAATAAAAATTGCTC 854
Qy      241 IleLYsProLYsThrAsnAlaPheGIuAlaIaLYsLYsGLyAsnTYrAlaLeuTrpMet 260
Db      855 ATCAAAACCAAAACCAATCCGTTGAGCTGCTCTATAAAGAAATTACCATTTGGAGATG 914
Qy      261 GIyProTYrLYsValSerLYsGLyIleLYsProThrgIuGLyLeuMetValAspPheSer 280
Db      915 GGGCGGTATTAAGTAAGCAAGAAAGAAATCAACCGAAGGATTAATGTCATTTCTCC 974
Qy      281 AspIleArqProTYrGIyAsnHisThrgIyAsnSerAlaProSerValGIuLYsAspAsn 300
Db      975 GATTATCCGGCCATACGGCAATATACGGGTAACTCCGCCCATCCGTAGAGCTGATAC 1034
Qy      301 SerHisGIuGLyTYrGIyTYrSerAspGIuAlaValArqGIuHisArqGIuGLyInPro 320
Db      1035 AGTCATGAGGGGTATGATACAGCGATGAGGAGTGCGCAACATAGCAAGGGCACTT 1094

RESULT 3
US-09-043-302-1
; Sequence 1, Application US/09043302
; Publication No. US20020086349A1
; GENERAL INFORMATION:
; APPLICANT: MEYER, Thomas F.
; APPLICANT: RUDEL, Thomas
; APPLICANT: SCHEUBERPLUG, Ina
; APPLICANT: MAIER, Jurgen
; APPLICANT: EICKERNJAGER, Sandra
; APPLICANT: SCHMANN, Thomas
; TITLE OF INVENTION: Nucleic Acid Molecules Encoding Proteins Which Impart
; FILE REFERENCE: 0147-172P
; CURRENT APPLICATION NUMBER: US/09/043,302
; EARLIER FILING DATE: 1998-06-08
; EARLIER APPLICATION NUMBER: PCT/EP96/04092
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 3287
; TYPE: DNA.
; ORGANISM: Neisseria gonorrhoeae
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (136)..(447)

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;
; NAME/KEY: CDS
; LOCATION: (583)..(1542)
;
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1585)..(3111)
US-09-043-302-1

Alignment Scores:
Pred. No.: 1,636-192 Length: 3287
Score: 1645.00 Matches: 320
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-10-617-835-4 (1-320) x US-09-043-302-1 (1-3287)

Qy      1 MetArgAlaArgLeuLeuIleProIleLeuPheSerValPheIleLeuSerAlaCysGIy 20
Db      583 ATGCGGGACGGCTCTGATACCTATCTTTTTCGTTTATTATTATCCGCTGGGG 642
Qy      21 ThrLeuThrgIyIleProSerHisGLyGLyLYsArqPheAlaValGIuGLyLeu 40
Db      643 ACACGACACGGATTCATCCATCGCATGGCGGAGCAACCGTTCGGGTGAAACAAAGATT 702
Qy      41 ValAlaAlaSerAlaArgAlaAlaValLYsAspMetAspLeuGLuAlaLeuHisGLyArg 60
Db      703 GTGGCGGCTTTCGCAGAGCTGCCCTTAAAGCATGAGATTTAACAGCATTAACAGCA 762
Qy      61 LYsValAlaLeuTYrIleAlaThrMetGLyAspGIuGLySerGIySerLeuThrgIy 80
Db      763 AAAGTTGCATTTGATTCATTCGACCTATGCGGACCAAGCTTCAGGAGTTTGACAGGGGT 822
Qy      81 ArgTYrSerIleAspAlaLeuIleArqGIyGLyTYrIleAsnSerProAlaValArgThr 100
Db      823 CGCTACTCATTTGATGACCTGATTCGGCGGAAATCATTAACAGCCCTGCCGCAAC 882
Qy      101 AapTYrThTYrProArqTYrGLuThrThraIaGIuThrThSergIyGLyLeuThrgIy 120
Db      883 GATTACACCTATCCCGGTACGAAACCAACCGTGAACAAACATCAAGCGGTGACGGGT 942
Qy      121 LeuThrThSergSerThrLeuAsnAlaProAlaLeuSerArqThrgIInserAspGly 140
Db      943 TTAAACCACTCTTTATCTACCTTAATAGCCCTGACCTCGCGCAACCCAAATCAACGGT 1002
Qy      141 SerGIySerArqSerSerLeuGLyLeuAsnIleGIyGLyMetGIyAspTYrArqAnglu 160
Db      1003 AGCGAAGTAGAGACAGCTGGGCTTAATATATGGCGGATGGGGATTATGAAATGA 1062
Qy      161 ThrLeuThrThAsnProArqAspThraIaPheLeuSerHisLeuValGIuThrValPhe 180
Db      1063 ACCTTGACACCAACCCCGCGACACTGCTTCTTCCCACTTGCTACAGACCGTATTT 1122
Qy      181 PheLeuArqGIyIleAspValIaSerProAlaAsnAlaAspThrAspValPheIleAsn 200
Db      1123 TTCCTGGCGGAGATAGACGTGTGTTCTCCTGCCAATGCCGATACAGATGTGTTATTAC 1182
Qy      201 IleAspValPheGIyThrIleArqAsnArqThrgIuMetHisLeuTYrAsnIaGIuThr 220
Db      1183 ATCGACGATTCGGAACGATACGCAACAGAACCGAAATGACCTATTAACAATCCGAAACA 1242
Qy      221 LeuLYsAlaGIuThrLYsLeuGLuTYrPheAlaValAspArqThrAsnLYsLYsLeuLeu 240
Db      1243 CTGAAGGCCCAAAACCTGAATATTTCCGAGTAGACAGAACCAATAAAAATTGCTC 1302
Qy      241 IleLYsProLYsThrAsnAlaPheGIuAlaIaLYsLYsGLyAsnTYrAlaLeuTrpMet 260
Db      1303 ATCAAAACCAAAACCAATCCGTTGACCTGCTTAAGAAATTAGCATTTGGAGATG 1362
Qy      261 GIyProTYrLYsValSerLYsGLyIleLYsProThrgIuGLyLeuMetValAspPheSer 280
Db      1363 GGGCGGTATTAAGTAAGCAAGAAATCAACGAGCAAGGATTAATGTCATTTCTCC 1422

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Oy 281 AsplleargProTYRGIYAsnHisThrGlyAsnSerAlaProSerValGluAlaAspAsn 300
Db 1423 GATATCCGGCCATACGGCAATCATTCGGGTAACTCCGCCCATCCGTGAGGCTGATTAAC 1482
Oy 301 SerHisGluGIYTYRGIYTYRSerAspGluAlaValArgInHisArgInGIYGLnPro 320
Db 1483 AGTCATGAGGGGTATGATGATACGCGATGAGCAGTGAACAAACATGACAAAGGGCAACT 1542

RESULT 4
US-10-617-835-1
; Sequence 1, Application US/10617835
; Publication No. US20050124037A1
; GENERAL INFORMATION:
; APPLICANT: MEYER, Thomas F.
; APPLICANT: RUDEL, Thomas
; APPLICANT: SCHUEBERPLOG, Ina
; APPLICANT: MAIER, Jurgen
; APPLICANT: EICKERMAYER, Sandra
; APPLICANT: SCHWAN, Thomas
; TITLE OF INVENTION: Nucleic Acid Molecules Encoding Proteins Which Impart
; TITLE OF INVENTION: the Adhesion of Neisseria Cells to Human Cells
; FILE REFERENCE: 0147-172P
; CURRENT APPLICATION NUMBER: US/10/617, 835
; PRIOR FILING DATE: 2003-07-14
; PRIOR APPLICATION NUMBER: US/09/043,302
; PRIOR FILING DATE: 1998-06-08
; PRIOR APPLICATION NUMBER: PCT/EP96/04092
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 3287
; TYPE: DNA
; ORGANISM: Neisseria gonorrhoeae
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (136)..(447)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (583)..(1542)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1585)..(3111)
US-10-617-835-1

Alignment Scores:
Pred. No.: 1,63e-192 Length: 3287
Score: 1645.00 Matches: 320
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 22 Gaps: 0

US-10-617-835-4 (1-320) x US-10-617-835-1 (1-3287)
Oy 1 MechArgAlaArgLeuLeuIleProIleLeuPheIleLeuSerAlaCysGIY 20
Db 583 ATGGGGGACCGGCTGCTGATACCTATTCTTTTCGGTTTATTATTATCCGCTCGGG 642
Oy 21 ThrLeuThrGIYIleProSerHisGIYGIYGIYIYsArgPheAlaValGluGlnGluLeu 40
Db 643 ACATGACAGAGTATTCATCCATGCGATGCGAGCAAAACCTTCGCGGTGGAACAAGAACTT 702
Oy 41 ValAlaAlaSerAlaArgAlaAlaValIYsAspMetAspLeuGlnAlaLeuHisGIYArg 60
Db 703 GTGGCCCGTTCTGCGAGGCTGCGGTAAAGACATGATTTTACAGGCATTTACAGGACGA 762
Oy 61 LysValAlaLeuTYRAlaIleThrMetGIYAspGlnGIYSerGIYSerLeuThrGIYGIY 80
Db 763 AAAGTTGATTTGATTCATTCGCAACTRATGGCGACCAAGTTTCAGGACATTTGACAGGGGT 822
Oy 81 ArgTYRSerIleAspAlaLeuIleArgGIYGIYTYRLeuSerProAlaValArgThr 100
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Db 823 CGTACTCCATTCATGATGACCTGATTCGGGGCAATATACATTAACAGCCCTCGCGCACCC 882
Oy 101 AspTYRThrTYRProArgTYRGIYThrThrAlaGluThrThrSerGIYGIYLeuThrGIY 120
Db 883 GATTACACCTATTCGGCTTACGAAACCAACCGCTTAACCAATCAAGGGGTGACGGGT 942
Oy 121 LeuThrThrSerLeuSerThrLeuAsnAlaProAlaLeuSerArgThrGlnSerAspGIY 140
Db 943 TTAACTCTCTTATATCTACACTTAATGCCCTTCCTGCACTCTGCCACCATCAGACGGT 1002
Oy 141 SerGlySerArgSerSerLeuGIYLeuAsnIleGIYIYMetGIYAspTYRArgAsnGlu 160
Db 1003 AGCGAAGTAGAGACAGACTGCTGGCTTAATATTTGGCGGATGGGGATTAATCGAAATGA 1062
Oy 161 ThrLeuThrThrAspProArgAspThrAlaPheLeuSerHisLeuValGlnThrValPhe 180
Db 1063 ACCTTGACGACCAACCCGCGGACACTGCTTCTTCCACTTGATGACAGACGGTATTT 1122
Oy 181 PheLeuArgGIYIleAspValValSerProAlaAsnAlaAspThrAspValPheIleAsn 200
Db 1123 TTCCTGGCGGCGCATAGAGTTGTTCTCTGCGCAATGCCATACAGATGTTATTATTAAC 1182
Oy 201 IleAspValPheGIYThrIleArgAsnArgThrGluMetHisLeuTYRAsnAlaGluThr 220
Db 1183 ATCGACGTAATTCGGAACGATACGCAACAGAACCCGAATTCACCTATCAATGCCGAAACA 1242
Oy 221 LeuysAlaGlnThrIYsLeuGIYTYRThrPheAlaValAspArgThrAsnIYsLeuLeu 240
Db 1243 CTGAAGCCCAACCAACCTGGAATATTTGCAGATGACAGAACCAATTAATTAATTTGCTC 1302
Oy 241 IleYsProIYsThrAsnAlaPheGluAlaAlaTYRGIYsGluAsnTYRAlaLeuTYRMet 260
Db 1303 ATCAAAACCAAAACCAATGGCTTTGAAAGCTGCTCTTAAGAAATTAACGATTTGTGATG 1362
Oy 261 GlyProTYRLeuValSerIYsGIYIleYsProThrGluGIYLeuMetValAspPheSer 280
Db 1363 GGGCGGTATTAAGTAAAGTAAAGGATCAAAACCGACGGAAGGATTAATGTCGATTTCTCC 1422
Oy 281 AsplleargProTYRGIYAsnHisThrGlyAsnSerAlaProSerValGluAlaAspAsn 300
Db 1423 GATATCCGGCCATACGGCAATCATTCGGGTAACTCCGCCCATCCGTGAGGCTGATTAAC 1482
Oy 301 SerHisGluGIYTYRGIYTYRSerAspGluAlaValArgInHisArgInGIYGLnPro 320
Db 1483 AGTCATGAGGGGTATGATGATACGCGATGAGCAGTGAACAAACATGACAAAGGGCAACT 1542

RESULT 5
US-10-320-800-69
; Sequence 69, Application US/10320800
; Publication No. US20030215469A1
; GENERAL INFORMATION:
; APPLICANT: ROBINSON, ANDREW
; APPLICANT: GORRINGE, ANDREW
; APPLICANT: HUDSON, MICHAEL
; APPLICANT: REDDIN, KAREN
; TITLE OF INVENTION: MULTICOMPONENT MENINGOCOCCAL VACCINE
; FILE REFERENCE: 1581.0790001
; CURRENT APPLICATION NUMBER: US/10/320, 800
; CURRENT FILING DATE: 2002-12-17
; PRIOR FILING DATE: PCT/GB99/03626
; PRIOR FILING DATE: 1999-11-02
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 69
; LENGTH: 939
; TYPE: DNA
; ORGANISM: Neisseria meningitidis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(939)
; OTHER INFORMATION: NMB0652 maf A
US-10-320-800-69
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Alignment Scores:

Pred. No.: 5,836-117 Length: 939
 Score: 1029.00 Matches: 197
 Percent Similarity: 76.34% Conservative: 49
 Best Local Similarity: 62.74% Mismatches: 62
 Query Match: 62.55% Indels: 6
 DB: 17 Gaps: 2

US-10-617-835-4 (1-320) x US-10-320-800-69 (1-939)

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QY 5 LeuLeuIleProIleLeuPheSerValPheIleLeuSerAlaCyGlyThrLeuThrGly 24
DB 16 CTCCTCATCCCTC-----GTCCTCAGCCCTGCGGCACTGACCGGCG 60

QY 25 IleProSerHieGlyGlyValArgPheAlaValGlnGlnIleValAlaIleSer 44
DB 61 ATACCGCGCCAGCGCGGCGCAACGCTTGCGGTGAAACAAGACTCGTCCCGCATG 120

QY 45 AlaArgAlaAlaValIlePhePheSerLeuGlnAlaLeuHieGlyValArgValAlaLeu 64
DB 121 TCCCGCGCGCGCTCAAAAGAAATGGATTGTCGCGCTAAAGAGACGCAAGCCGCTT 180

QY 65 TyrIleAlaThrMetGlyValArgGlnIleSerGlySerLeuThrGlyValArgTyrSerIle 84
DB 181 TACGCTCGCTATGGCGACCAAGGCTGCGGACATAGCGCGGACGCTATCTATC 240

QY 85 AspAlaLeuIleArgGlyGlyTyrIleAsnSerProAlaValArgThrAspTyrThrTyr 104
DB 241 GACGCACTGATACGGCGGCGCTACCAACAACCCGAAAGTGGCCACCAATACAGTAC 300

QY 105 ProArgTyrGlnThrThrAlaGlnThrThrSerGlyGlyLeuThrGlyLeuThrThrSer 124
DB 301 CCCGCTACGACACTACCCGCCAACCAATCCGACGCGCTCCAGCGTACCACTTCC 360

QY 125 LeuSerThrLeuAsnAlaProAlaLeuSerArgThrGlnSerAspGlySerGlySerArg 144
DB 361 ACATGCGCTTTGAAAGCCCCCGCGCGCTGACCAAAAACGCCGAGCAAAAGCGCA 420

QY 145 SerSerLeuGlyLeuAsnIleGlyGlyMetGlyAspTyrArgAsnGlnThrLeuThrThr 164
DB 421 CGCTCGCGCGGACGTGCGCTCAACGCGGCGGACGTACCGCAAGAAACCTGCGCGC 480

QY 165 AsnProArgAspThrAlaPheLeuSerHieValGlnThrValPhePheLeuArgGly 184
DB 481 AACCCCGCGGACGTTCCTCTCTGACCAACCTCATCAAAACGCTCTTCACTGCGCGC 540

QY 185 IleAspValIleSerProAlaAsnAlaAspThrAspValPheIleAsnIleAspValPhe 204
DB 541 ATCGAAAGTGTACCGCCGCAATACGCGGACCGGACGTATGTGTAACCGTCAAGTATC 600

QY 205 GlyThrIleArgAsnArgThrGlnMetHieValArgAlaGlnThrLeuValAsn 224
DB 601 GGCACGCGTCGCGGCGGTACCGCACTGCACTCTACAAACCGGAAACCTTAAAGCCAA 660

QY 225 ThrIleValGlnTyrPheAlaValAspArgThrAsnIleValLeuLeuIleLeuPheProIys 244
DB 661 ACCAAGCTCGAAATATTTCCCGCTGACCGGACGCGGAAACGTGTGTTACCCCTTAA 720

QY 245 ThrAsnAlaPheGlnAlaAlaTyrIleValAsnTyrAlaLeuThrMetGlyProTyrIle 264
DB 721 ACCCGCGCTTACGATACCCCAATACCAAGAACATACGCGCTTGAACGCGGCTTACAA 780

QY 265 ValSerIleGlyIleValProThrGlnGlyLeuMetValAspPheSerAspIleArgPro 284
DB 781 GTACAGAAACCGCTCAAGCGCTGACGCGCTGATGTGATTTCTCCGACATTAACCCC 840

QY 285 TyrGlyAsnHieThrGlyAsnSerAlaProSerValGlnAlaAspAsnSerHieGlnGly 304
DB 841 TACGGGACAAACCGCCCAAAACGCTCCGACTTCAAAACAAACGATTAACAAACCC 900

QY 305 TyrGlyTyrSerAspGlnAlaValArgGlnHieArgGlnGly 318
DB 305 TyrGlyTyrSerAspGlnAlaValArgGlnHieArgGlnGly 318

```

DB 901 ---GATGTCGCAAGCAACTCATCCGCGCGCGCAAGAGCA 939

RESULT 6

US-10-156-761-1/c

Sequence 1, Application US/10156761
 Publication No. US20030119018A1
 GENERAL INFORMATION:

APPLICANT: OMURA, SATOSHI
 APPLICANT: IKEDA, HARUO
 APPLICANT: ISHIKAWA, JUN
 APPLICANT: HORIKAWA, HIROSHI
 APPLICANT: SHIBA, TADAYOSHI
 APPLICANT: SAKAKI, YOSHIYUKI
 APPLICANT: HATTORI, MASAHIRA
 TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
 FILE REFERENCE: 249-262
 CURRENT APPLICATION NUMBER: US/10/156,761
 PRIOR FILING DATE: 2002-05-29
 PRIOR APPLICATION NUMBER: JP 2001-204089
 PRIOR FILING DATE: 2001-05-30
 PRIOR APPLICATION NUMBER: JP 2001-272697
 PRIOR FILING DATE: 2001-08-02
 NUMBER OF SEQ ID NOS: 15109
 SEQ ID NO 1
 LENGTH: 9025608
 TYPE: DNA
 ORGANISM: Streptomyces avermitilis
 FEATURE:
 NAME/KEY: misc feature
 LOCATION: (4187715)
 OTHER INFORMATION: a, c, g, other or unknown
 US-10-156-761-1

Alignment Scores:

Pred. No.: 1,316+04 Length: 9025608
 Score: 107.50 Matches: 50
 Percent Similarity: 42.47% Conservative: 29
 Best Local Similarity: 26.88% Mismatches: 52
 Query Match: 6.53% Indels: 55
 DB: 15 Gaps: 10

US-10-617-835-4 (1-320) x US-10-156-761-1 (1-9025608)

```

QY 6 LeuIleProIleLeuPheSerVal-----PheIleLeuSerAlaCyGlyThrLeuThr 23
DB 8122195 CTGTCGCGCTGTGTCGCGCGCGTGCAGCGCGCGCGTGCAGCGCGCG 8122136

QY 24 GlyIleProSerHieGlyGly-----GlyValArg----- 33
DB 8122135 GGCACCCCAAGCGGAGACGCGCGGTGAGCTTCGCGGCGCGCGCGCGCGCG 8122076

QY 34 -----PheAlaValGlnGlnIleu 40
DB 8122075 CTGCGACCACTGGAGCTCCAGCTGGGTACGACACTCAAGCTGCGGTATCAGGAAATAT 8122016

QY 41 ValAlaIleSerAlaArgAlaValIleValAspMetAsp----- 53
DB 8122015 CCCGCGGAGCC-----GCTGCACCTGCTGACGTGAGCGCAATGCGGTGATGTGTG 8121962

QY 54 -----LeuGlnAlaLeuHieGlyArgValAlaIleValIleValThr 68
DB 8121961 CATCGCGGACATGCGACTTCGACACTGATGTCG-----CTCAACTCTTCGCGG 8121911

QY 69 MetGlyAspGlnGlySerGlySerLeuThrGlyIleArgTyrSerIleAspAlaLeuIle 88
DB 8121910 GTCGGTGTGCTTCGCCAGGTGAGACACTGCGCGCGGTGTGCTGTCACCTTAACG 8121851

QY 89 ArgGlyGlnTyrIleAsnSer-----ProAlaValArgThrAspTyrThrTyrPro 105
DB 8121850 GCACCTTCGTGATGATACCTCGCGGAGACTCGCCCATTCGATCGCAGCGCGATC--- 8121794

QY 106 ArgTyrGlnThrThrAlaGlnThrThrSerGlyGlyLeuThrGlyLeuThrThrSerLeu 125
DB 106 ArgTyrGlnThrThrAlaGlnThrThrSerGlyGlyLeuThrGlyLeuThrThrSerLeu 125

```

Db 8121793 -----ACGGCTGCTCCACCTGCTGTCACAGGAGCGGTGCGCGGTC---ACGGCTTGG 8121746
Qy 126 SerThiLeuAsnAlaPro-----AlaLeuSerArgThrGlnSerAspGly 140
Db 8121745 GCGACGGCCACACGCGCGCTGTGCACGGTGAAGCGCGCGCGCGCATCCAGCACGGGC 8121686
Qy 141 SerGlySerArgSerSer 146
Db 8121685 CAGGGGTGCGCGCTGCGCGC 8121668

RESULT 7
US-10-398-221-10
; Sequence 10, Application US/10398221
; Publication No. US20040018514A1
; GENERAL INFORMATION:
; APPLICANT: KUNST, Frederick
; APPLICANT: GLASER, Philippe
; TITLE OF INVENTION: Listeria innocua, genome and applications
; FILE REFERENCE: 344 702 - US
; CURRENT APPLICATION NUMBER: US/10/398,221
; PRIOR FILING DATE: 2003-03-27
; PRIOR APPLICATION NUMBER: PCT/FR 01/03 061
; PRIOR FILING DATE: 2001-10-04
; PRIOR APPLICATION NUMBER: FR 00/12 697
; PRIOR FILING DATE: 2000-10-04
; NUMBER OF SEQ ID NOS: 4025
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 10
; LENGTH: 1163020
; TYPE: DNA
; ORGANISM: Listeria innocua
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(end)
; OTHER INFORMATION: n can be any nucleotide: a, g, c or t/u
US-10-398-221-10

Alignment Scores:
Pred. No.: 1.35e+03 Length: 1163020
Score: 104.50 Matches: 77
Percent Similarity: 35.24% Conservative: 40
Best Local Similarity: 23.19% Mismatches: 113
Query Match: 6.35% Indels: 102
DB: 17 Gaps: 16
US-10-617-835-4 (1-320) x US-10-398-221-10 (1-1163020)

Qy 9 IleLeuPheSerValPheIleuSerAlaCys-GlyThrLeuThrGlyIleProSerHi 28
Db 62741 ATTTTATCTCGAGGCTGGAATTAAGTAGCTGCGGGAACAGACACTGCATTGCCAGA-- 62798
Qy 28 sGlyGlyGlyAsnArgPheAlaValGlnGlnLeuValAlaIleSerAlaArgAlaAl 48
Db 62799 -----CTTTCCAAAGCGGCTGAAAAAC 62821
Qy 48 aValIleAspMetAspLeuGlnAlaLeuHiGlyArgIleValAlaLeuTyrIleAlaTh 68
Db 62822 GAATTAAGATGACATGCTGCTGCCTACCTATGCGGCAAAACATGAATAACCCATTAATAAC 62881
Qy 68 rMetGlyAspGlnGlySerGlySerLeuThrGlyGlyArgTyr-----SerIleAs 85
Db 62882 T-----GGTGTATGGGGCGCGTGTGTGAGATTGGCGGTATGAGATATTGA 62929
Qy 85 Palaleu-----11eArgGlyGly 91
Db 62930 TGCTGTAAAGCCAAAGCCCACTTTAAAGATATTGGAGTACTGCCAAAGCCGC 62989
Qy 91 uTyrIleAsnSerProAlaValArgThrAspTyrThrTyrProArgTyrGluThrThrAl 111
Db 62990 GTATCTTATATGTAAGAAACGCGGAGTTTATACATAT----- 63029
Qy 111 aGluThrThrSerGlyGlyLeuThrGlyLeuThrThrSerLeuSerThrLeuAsnAlaPr 131

Db 63029 ----- 63029
Qy 131 oAlaLeuSerArgThrGlnSerAspGlySerArgSerLeuGlyLeuAsnI 151
Db 63030 -----GACATATCGGGTTCATATTGCTATAGGCACAGATGTAAAGATTAATATCT 63082
Qy 151 eGlyGlyMetGlyAspTyr-----ArgAsnGluThrLeuThrThrAsnProArgAs 168
Db 63083 AGGTGGATGATTTCTTGATGACAGTGCAGATGAATAACACGACTTCACATTAAGCGCGA 63142
Qy 168 pThrAlaPheLeuSerHiLeuValGlnThrValPhePheLeuArgGlyIleAspValVa 188
Db 63143 TGAA-----CTTCAAAAGGCTATTAAACCGGATTTGTC-----GGTACAGTGCAT 63190
Qy 188 lSerProAlaAsnAlaAspThrAspValPheIleAsnIleAspValPheGlyThrIleAr 208
Db 63191 C---CCGAAACCAATCA-----TATGCCAATTATATGTGGTACACTGTAA 63241
Qy 208 gAsnArgThrGlnMetHiLeuTyrAsnAlaGluThrLeuValaGlnThrIleLeuG 228
Db 63242 ACCTTATAGTAAATGAGTCGATACGAAATTAACGATTACTATATGAAAA----- 63296
Qy 228 uTyrPheAlaValAspArgThrAsnIleGlyLeuLeuIleGlyProIleThrAsnAlaPh 248
Db 63297 -----GCGGATGAAACAAATGA-----GTCTTGAAATCAACAGAGCTATCTT 63340
Qy 248 eGluAlaAla-----TyrIleGluAsnTyrAlaLeuTyrPme 260
Db 63341 TGAAACGTAATAATTACCTTAAGTTTATTTCCAGTAAACCGCGCAACGCTTACTGC 63400
Qy 260 rGlyProTyrIleValSerIleGlyIleGlyProThrGlnGly-----LeuMetValAs 278
Db 63401 TGAAGATTATTAACA-----GGTACGGTTACTACTGAGTGGCAATACAGATGTGA 63454
Qy 278 pPheSerAspIle-----ArgProTyrGlyAlaAsnHisTh 289
Db 63455 TTTAGCTTGGGTGATGATGACAGCAAAATCCGCAAGCGCATCTTACTTCCCGCTT 63514
Qy 289 rGlyAsnSerAlaProSerValGluAlaAspAsn 300
Db 63515 AAAATCGATGCACTGTGTTGATGTAAATAT 63548

RESULT 8
US-10-398-221-2058
; Sequence 2058, Application US/10398221
; Publication No. US20040018514A1
; GENERAL INFORMATION:
; APPLICANT: KUNST, Frederick
; APPLICANT: GLASER, Philippe
; TITLE OF INVENTION: Listeria innocua, genome and applications
; FILE REFERENCE: 344 702 - US
; CURRENT APPLICATION NUMBER: US/10/398,221
; PRIOR FILING DATE: 2003-03-27
; PRIOR APPLICATION NUMBER: PCT/FR 01/03 061
; PRIOR FILING DATE: 2001-10-04
; PRIOR APPLICATION NUMBER: FR 00/12 697
; PRIOR FILING DATE: 2000-10-04
; NUMBER OF SEQ ID NOS: 4025
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2058
; LENGTH: 3011208
; TYPE: DNA
; ORGANISM: Listeria innocua
US-10-398-221-2058

Alignment Scores:
Pred. No.: 5.78e+03 Length: 3011208
Score: 104.50 Matches: 77
Percent Similarity: 35.24% Conservative: 40
Best Local Similarity: 23.19% Mismatches: 113
Query Match: 6.35% Indels: 102
DB: 17 Gaps: 16

US-10-617-835-4 (1-320) x US-10-398-221-2058 (1-3011208)

```

OY      9  IleuPheSerValPheIleuSerAlaCys-GlyThrLeuThrGlyIleProSerHi 28
DB      146982 ATTTATACTCGAGCGCTGGATAAAGTAGACTCGCGAACAACAGACACTGCTGCCAGGA-- 147039
OY      28  eGlyGlyGlyValArgPheAlaValGluGluIleuValAlaIleSerAlaArgAlaAl 48
DB      147040 -----CTTTCCAGCGCGTGAAGAAAAC 147062
OY      48  aValIysaPheMetAPLeuGlnAlaLeuHiGlyArgValAlaLeuTyrIleAlaTh 68
DB      147063 GAATTAAGATGCAATGCGTCTCCCTCATGCGGCAAAACATGAAGAACCAATTAAAC 147122
OY      68  rMetGlyaPheGlnGlySerGlySerLeuThrGlyGlyArgTyr-----SerIleAs 85
DB      147123 T-----GGTAGTGGGGCGCGTGTGCGAGTGTGGCGGTATAGAAATATGCA 147170
OY      85  PAlaLeu-----IleArgGlyGly 91
DB      147171 TGCTCTAAAGCCCAAGACCCCACTTTAAAGAAATATGGGATGATCTGCCAAGCGCC 147230
OY      91  uTyrIleAsnSerProAlaValAlaArgThrAspTyrThrTyrProArgTyrGluThrThrAl 111
DB      147231 GTATCTTATATAGTAAGAAACAGCGGAGTTTACACATAT----- 147270
OY      111  aGluThrThrSerGlyGlyLeuThrGlyLeuThrThrSerLeuSerThrLeuAsnAlaPr 131
DB      147270 ----- 147270
OY      131  oAlaLeuSerArgThrGlnSerPheGlySerGlySerArgSerSerLeuGlyLeuAsnI 151
DB      147271 -----GACAAATACGCGCTTCAATGCTATAGACACGATGTAAAGATAATATATCT 147323
OY      151  eGlyGlyMetGlyArgTyr-----ArgAsnGluThrLeuThrThrAsnProArgAs 168
DB      147324 AGTGGGATGATTTCTTGATGATCGACGCGAGATTAACACGACTTCACTCAACCGCA 147383
OY      168  rThrAlaPheLeuSerHiLeuValGlnThrValPhePheLeuArgGlyIleAspValVa 188
DB      147384 TGAA-----CTTACAAAGCGCTATTAAACCGGATTTGTC-----GGTACAAAGTCAT 147431
OY      188  lSerProAlaAsnAlaAspThrAspValPheIleAsnIleAspValPheGlyThrIleAr 208
DB      147432 C---CCGCAAAACGCAATCACA-----TATCGAATTTAAATGTGTAGCAACCTGTAA 147482
OY      208  gAsnArgThrGluMetHiLeuTyrAsnAlaGluThrLeuValAlaGlnThrIleLeuGl 228
DB      147483 ACCTTATAGTGAATAATGAGCTCGATACGAATTCGATTTACTAATATGAABAA----- 147537
OY      228  uTyrPheAlaValAlaAspArgThrAsnIleValLeuLeuIleValProIleThrAsnAlaPh 248
DB      147538 -----GCGGATGAACAAATGAA-----GTCTGAATGATCAACAGAGCTATCTTT 147581
OY      248  eGluAlaAla-----TyrIysGluuantiYrAlaLeuTyrPme 260
DB      147582 TGAACAGTAAATTAACCTAAGTTTATATTCAGTAAAGCGCGAAGCCCTACTGTC 147641
OY      260  tGlyProTyrIleValSerIleGlyIleValProThrGluGly-----LeuMetValAs 278
DB      147642 TGGAAATTAATAAGCA-----GTTACGCTTACTCTTCAAGTGGCAATACAGTATGCA 147695
OY      278  pPheSerAspIle-----ArgProTyrGlyAsnHiIerTh 289
DB      147696 TTACTCTTCGCTGATGATGACACAGCAATTCGCAAGCGCATTTATACTTCGCTT 147755
OY      289  rGlyAsnSerAlaProSerValGluAlaAspAsn 300
DB      147756 AAAATCGAGTCACTCTAGTGTGATGTAAATAT 147789

```

RESULT 9
US-10-437-963-87357
; Sequence 87357, Application US/10437963

Publication No. US20040123343A1

```

; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 87357
; LENGTH: 2604
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MKT4530_8630C.1
; US-10-437-963-87357

Alignment Scores:
Pred. No.: 0.161 Length: 2604
Score: 103.50 Matches: 86
Percent Similarity: 34.66% Conservative: 53
Best Local Similarity: 21.45% Mismatches: 129
Query Match: 6.29% Indels: 133
DB: 19 Gaps: 20

US-10-617-835-4 (1-320) x US-10-437-963-87357 (1-2604)

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```

OY      19  CysGly--ThrLeuThrGlyIleProSerHiGlyGlyGlyLeu-----ArgPhe 34
DB      274  TGTGCTGCTGCTTATGATGATGGCTACACGATACCGGACCGACAGGAGATTACTCAGGTTCC 333
OY      35  AlavalGluGlnGluLeuVal----- 41
DB      334  GCCGACCCGACGCCGCGCATGCTGCCAGATGACGCCGCGACCCAGCTCCGCCCTTCC 393
OY      42  AlaAlaSerAlaArgAlaAlaVal----- 49
DB      394  TTCACGCGCTGAGGCGCGCTCAGCTCGGGGACCGAACACCGACGAGCTGGAGTTCC 453
OY      50  ----- 54
DB      454  ATCTCGACGAGTGCCTCACTATATACGCGCATGCTCATAGGAGAGAGACTTGAT--- 510
OY      55  GluAlaLeuHiGlyArgGlyValAlaLeuTyrIleAlaThrMetGlyAspGlnGlySer 74
DB      511  -----GAGAAAGCTCAGCATGATAC-----CAGGAGGAGTCC 540
OY      75  GlySerLeu-----ThrGlyIleArgTyr----- 82
DB      541  GCGGCGCTCCGCGCTGCTCGCAAGCATTTATGACATTTTGGCACAGTTCCCGCC 600
OY      83  SerIleAspAlaLeuIleArgGlyGluTyrIleAsnSerProAlaValAlaArgThrAspTyr 102
DB      601  TCCCTGACCGGACGAGCTGTAGCTTGCGCCCTCGACACCGCGAGTGAAGTATGACACTGAC 660
OY      103  ThrTyrProArgTyrGluThrThrAlaGluThrThrSerGlyGlyLeuThrGlyLeuThr 122
DB      661  AGCTATCCA---CACTCTTGAGTGTCTGTATACACAGCAATTAAGTGTGCGCTC 717
OY      123  ThrSerLeuSerThrLeuAsnAlaProAlaLeuSerArgThrGlnSerAspGlySerGly 142
DB      718  GATAC-----ACCAACCGCTTATGTTGACACAGT 750
OY      143  SerArgSerSerLeuGlyLeuAsn-----IleGlyIleMetGlyAspTyr 157
DB      751  GAGTATCGAGCTGTGTGCTCATTTCTCAACCGCGGTGGCCATCAAGTATGATGT 810

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QY 158 ArgAsn-----GluThrLeuThrAspProArgAspThrAlaPhe 171
      |||
      |||
      |||
Db 811 GCGAAGCGATGAGACACTAGAGATCCTTGATTAGTAAGGACAGATCCCTGATAT 870
QY 172 LeuSerHisLeuValGlnThrValPhePheLeuArgGlyIleAspValValSerProAla 191
      |||
      |||
      |||
Db 871 TTGTTTGAGAGCTTCCACATGGGATTTGAGAGAGGTGTGACAGGACAGAGTTT 930
QY 192 AsnAlaAspThrAsp---ValPheIleAsnIleAspValPheGlyThrIleArgAsnArg 210
      |||
      |||
      |||
Db 931 CTCGCCGGGTAGCGATAGGTAGTGTATGATTAGAGGCTGTGTGTCGCAAAAGCTCA 990
QY 211 -----ThrGluMetHisLeuTyraAsnAlaGluThrLeuIleValGln--- 224
      |||
      |||
      |||
Db 991 GAAGCAGGGAAGATATTTCTGTGAATGCACAGCAAGCAGAGCTTTGAGGTAAAGAAA 1050
QY 225 -----ThyIleuGluIuTyrPhe 230
      |||
      |||
      |||
Db 1051 AACAGACAGAGTGAAGACCTTGACGTGATGGAAGACGGAATATGAAACAGTCTGCATTT 1110
QY 231 AlaValAsp-----ArgThrAsnIle 237
      |||
      |||
      |||
Db 1111 TGTTCGTGTAACCTGATTTGATGATGTTGATGTTCTGCTTCGCAAACTGAGAAG 1170
QY 238 LysLeuLeuIleLysProLysThrAsnAlaPheGluAlaAlaTyrlsGluAsnTyrla 257
      |||
      |||
      |||
Db 1171 AAGGCACTGATCTTCGAAAAATGATGCGTTTGAAGGCTCCAAAGATTCGCCCTTGCT 1230
QY 258 LeuTrpMetGlyProTyrlsVal---SerIleGlyIleLysProThrGluGlyLeuMet 276
      |||
      |||
      |||
Db 1231 CAGCCAAAGACGCAAGTGGGACCCGATCACGCGGACGGAACGCAACTAAG----- 1281
QY 277 ValAspPheSerAspIleArgProTyrlsAsnHisThrGlyAsnSerAlaProSerVal 296
      |||
      |||
      |||
Db 1282 AAGGATGGGTGGACCTTAGGACGCTACTCATCCAC-----TGTCCTCAGGCACTG 1332
QY 297 GluAlaAspAsnSerHisGluGlyTyrlsGlyTyrlsSerAspGluAlaValArgGlnHisArg 316
      |||
      |||
      |||
Db 1333 GCAGCTGATGACCGCGGACT-----GCTAATGAGTCTTAAAGCAATAAAG 1380
QY 317 Gln 317
      |||
      |||
      |||
Db 1381 CAG 1383

RESULT 10
US-10-122A-16487
; Sequence 16487, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: EUTRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335

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; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16487
; LENGTH: 1335
; TYPE: DNA
; ORGANISM: Clostridium botulinum
US-10-282-122A-16487

Alignment Scores:
Pred. No.: 0.118 Length: 1335
Score: 101.00 Matches: 71
Percent Similarity: 35.99% Conservative: 42
Best Local Similarity: 22.61% Mismatches: 111
Query Match: 6.14% Indels: 90
DB: 17 Gaps: 15

US-10-617-835-4 (1-320) x US-10-282-122A-16487 (1-1335)
QY 62 ValAlaLeuTyrlleAlaThrMetGlyAspGlnGlySerGly----- 75
      |||
      |||
      |||
Db 133 ATACCTTTTATGATATCTTAATA-----GTTCTGAGATTCGACTATATATA 183
QY 76 SerLeuThrGlyGlyArgTyrlsSerIleAspAlaLeuIleArgGlyIuTyrlleAsnSer 95
      |||
      |||
      |||
Db 184 TCTGTAACTCAAGCAGTAAGAAAGCAATATAGCTTGTGTAATAAAGCATATTAAACATA 243
QY 96 ProAlaValArgThrAspTyrlsThrTyrlsProArgTyrlsGluThrThrAlaGluThrThrSer 115
      |||
      |||
      |||
Db 244 TCCTTAGATTCTAAAAAAGTAAATAATTAATATATGAAAAAGATTATTAGTTAAGGGT 303
QY 116 -----GlyGlyLeuThrGlyLeuThrThrSerLeuSer----- 126
      |||
      |||
      |||
Db 304 CTTAAAAATAGTTGCTATAGGTGAGAGAACTGGCTTATCTATCTATGTTAAAGAACTTAAA 363
QY 127 -----ThrLeuAsnAlaProAlaLeuSerArgThrGlnSerAspGlySerGlySer--- 143
      |||
      |||
      |||
Db 364 TATATATACCTCTATATATTAACAGCTATATGTAACAGTGCAGATGATGGGGATCTGCT 423
QY 144 -----ArgSerSerLeuGlyLeuAsnIleGlyGlyMetGlyAspTyrlsArgAsnGluThr 161
      |||
      |||
      |||
Db 424 GAATTAAGAGAAAGATTATGACATGTTA-----CTTCACAGAGATATTAAGAACTGTATA 477
QY 162 LeuThrThrAspProArgAspThrAlaPheLeuSerHisLeuValGlnThrValPhe--- 180
      |||
      |||
      |||
Db 478 TTATCTTTATCAGATACAGAA---CCTTTAATGAGAGAACTTTTACAATATAGATTACA 534
QY 181 -----PheLeuArgGlyIleAspVal 188
      |||
      |||
      |||
Db 535 GATGAGAGACTTAAAAACAAAGTTTGTATTTATTTTACGTGTATGATGATGATATA 594
QY 189 Ser----- 189
      |||
      |||
      |||
Db 595 TCTAATATTTTGAAGACAGTTCAAAAAGTTAGTTGCTTTGGCTGTACAGAGAAA 654
QY 190 -----ProAlaAsnAlaAspThrAspValPheIleAsnIleAspValPheGlyThrIle 207
      |||
      |||
      |||
Db 655 GTTGATCCAGTAACCTTAGAG-----NATITAGTGTCTAAAGCTAGGCTG 699
QY 208 ArgAsnArgThr-----GluMetHisLeuTyrlsAsnAlaGluThrLeuTyrlsAla 223

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Oy      136  ThhGlnSerAspGlySerGlySerGlySer-----LeuGlyLeuAsnIleGlyGly 153
Db      652  ACTAGTTCACCTGGTGTGTGTATGCTGTATATTCACATTCATCATGAAACTCTGTGTGCA 711
Oy      154  MetGlyAspPyrZnArgAsnGlnThrLeuThrThiAsnProArgAspThrAlaPheLeuSer 173
Db      712  GTTTTGGCTCAGCTGACGGGTGAATTCAGCAGCAACCAAAATGACACA-----758
Oy      174  HisLeuValGlnThrValPhePheLeuArgGlyIleAspValSerProHisAsnAla 193
Db      760  -----GCAGGTGCA 768
Oy      194  AspThrAspValPheIle 199
Db      769  GACATGATGATTCATT 786

RESULT 14
US-10-282-122A-19283
Sequence 19283, Application US/10282122A
Publication No. US20040029129A1
GENERAL INFORMATION:
APPLICANT: Wang, Lianguu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zykkind, Judith
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
APPLICANT: Carr, Grant
APPLICANT: Yamamoto, Robert
APPLICANT: Forsyth, R.
APPLICANT: Xu, H.
TITLE OR INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITTA.034A
CURRENT APPLICATION NUMBER: US/10/282.122A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-09-09
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
SEQ ID NO 19283
LENGTH: 2622
TYPE: DNA
ORGANISM: Enterobacter cloacae
US-10-282-122A-19283

Alignment Scores:
Pred. No.: 0.588 Length: 2622
Score: 99.00 Matches: 64
Percent Similarity: 38.49% Conservative: 53
Best Local Similarity: 21.05% Mismatches: 147
Query Match: 6.02% Indels: 40

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QY      48 AlaValLysArgMetAspLeuGlnAlaLeuHisGlyArgLysValAlaLeuTyrIleAla 67
      202 ACGGTCGCCAGCGCGCATCTGCGGGTCTGAAGAAGCGGACGCGACGCTGACGGGTGAGAC 261
QY      68 ThrMetGlyAspGlnGlySerGlySerLeuThrGlnGlyArgTyrSerIleAspAlaLeu 87
      262 GTCACCAACGTTAAAGCAACAGCCGCTCGCGGGCGCGGAGTACAGCTGAGTGCACAC 321
QY      88 IleArgGlyLysTyrIleAsnSerProAlaValArgThrAspTyrThrTyrProArgTyr 107
      322 GCGCGCGTCGTCACCATCAATCTCGCG-----ACCGACGATATCTGAACCGCGCG 375
QY      108 GluThrThrAlaGluThrThrSerGlyGlyLeuThr-----GlyLeuThrThr 123
      376 GAAGCGAAGAGCGATCTGACCGTATCCGGCACACCGCGGACCGCGGCGGACGCGTGC 435
QY      124 SerLeuSerThrLeuAsnAlaProAlaLeuSerArgThrGlnSerAspGlySerGlySer 143
      436 ACCGATGCGCTGACAGCGCAAGACTAACACCAACCGTACGCGACGCGCGCTGAGAG 495
QY      144 ArgSerSerLeuGlyLeuAsnIleGlyGlyMetGlyAspTyrArgAsnGluThrLeuThr 163
      496 CTGAACGTCGCGCGCGCGCATCTGGCTGATTACCGAC---GGACGCGTCAACCGTTACC 552
QY      164 ThrAsnProArgAsp-----ThrAlaPheLeuSerHisLeuValGlnThrVal 179
      553 GCATCGTCAGCGCAAGCGGCAACCGCGCGTGGTGGTGCATCAACATTCG----- 603
QY      180 PhePheLeuArgGlyIleAspValValSerProAlaAsnAlaAspThrAspValPheIle 199
      604 -----GCGGTAGATATTCACCGCGCGCTGCG-----GTGACCATC 636
QY      200 AsnIleAspValPheGlyThrIleArgAsnArgThrGlnMetHisLeuTyrAsnAlaGlu 219
      637 AATACCGTGGCGGGGAGCATGTATTATTAATCGGAGAA-----CACGGCACGGCG 687
QY      220 ThrLeuLysAlaGlnThrLysLeuGluTyrPheAlaValAspArgThrAsnLysLeu 239
      688 CAGATCATTCAGCGGCAACCGCGCGCGGCGGAGGATAGGTGACCGTCAACCATC 747
QY      240 LeuIleLysProLysThrAsnAlaPheGlnAlaIleTyrLysGluAsnTyrAlaLeuTyr 259
      748 GCGGCGCAACCTTACACCAACCGTGTGGTGGTGGCG-----GGGAACTGGAGCGTGGCG 801
QY      260 MetGlyProTyrLysValSerLysGlyIleLysProThrGluGlyLeuMetValAspPhe 279
      802 GTA---CGGCGAGGCTGATTCCGCGCTC-----AGCGAGCGGACCGTAAACCGTCACT 852
QY      280 SerAspIleAspGlyProTyrGlyAsnHisThrGlyAsnSerAlaProSerValGluAlaAsp 299
      853 GCGTCGCTACAGCGCGCGCGGCAACCGGTACCGGACGCAATGACGTGACCGTGTAT 912
QY      300 AsnSerHisGluGlyTyrGlyTyrSer-----AspGluAlaValArgLysHis 315
      913 ACCGCTTCGCGCATTCGCTGCGCTTCAACCGCATACGAGTGAACAGTCTCTGAACCGGTA 972
QY      316 ArgGlnGlyGln 319
      973 GAAAAAAGTCAAG 984
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RESULT 15
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; Sequence 69, Application US/10146772
; Publication No. US20030124698A1
; GENERAL INFORMATION:

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; APPLICANT: Short, Jay
; APPLICANT: Weiner, David
; APPLICANT: Chaplin, Jennifer
; APPLICANT: Chi, Ellen
; APPLICANT: Milan, Aileen
; APPLICANT: Desantis, Gesa
; APPLICANT: Madden, Mark
; APPLICANT: Burk, Mark
; TITLE OF INVENTION: Nitriases
; FILE REFERENCE: Docket No. US20030124698A1 DIV-013US
; CURRENT APPLICATION NUMBER: US/10/146,772
; PRIOR FILING DATE: 2002-05-15
; PRIOR APPLICATION NUMBER: US 60/309,006
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US 60/351,336
; PRIOR FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: US 60/300,189
; PRIOR FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: US 09/751,299
; PRIOR FILING DATE: 2000-12-28
; PRIOR APPLICATION NUMBER: US 60/254,414
; PRIOR FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: US 60/173,609
; PRIOR FILING DATE: 1999-12-29
; NUMBER OF SEQ ID NOS: 386
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 69
; LENGTH: 939
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Obtained from an environmental sample
US-10-146-772-69

Alignment Scores:
Pred. No.: 0.141
Score: 98.50
Percent Similarity: 35.20%
Best Local Similarity: 22.74%
Query Match: 5.99%
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      876 GCGGCTGTAATGCGCGGACGAGTCAAA----- 850
QY      67 AlaThrMetGlyAspGlnGlySerGlySerLeuThrGlnGlyArgTyrSerIleAspAla 86
      849 CCAGCGCTTGGCATGCAAGCGCGCGTGCAGTCAAGTGGGGAACAGATCCCTCCG 790
QY      87 LeuIleArg-GlyGlyTyrIleAsnSerProAlaVal----- 98
      879 ATCGTAGAGCGCGCGCGGATTAACCTGCGCCAGGAGGCTGACGATCGCGCATCGT 730
QY      99 ArgThrAspTyrThrTyrProArgTyrGluThrThrAlaGluThrThrSerGlyGlyLe 118
      729 GCGCGCAACACCTCTTGGCCCGGGGTAAGCTCAACGGGGAATGTCGGGGAACGGGA 670
QY      118 ThrGlyLeuThrThrSerLeuSerThrLeuAsnAla-ProAlaLeuSerArgThrGlns 138
      669 CGCGCGGATGAACCTCGCGCACCGACGACGACGACCGCGCGCATCGCGATGT---- 614
QY      138 eAspGlySerGlySerArgSerSer-LeuGlyLeuAsnIleGlyGlyMetGlyAspTyr 157
      613 -----GCGCATGCTCGGAGCGCACCGCTCGGAGTC---ATCGGC----- 577
QY      158 ArgAsnGluThrLeuThrThrAsnProArgAspThrAlaPheLeuSerHisLeuValGln 177

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Qy 178 ThrValPhePheLeuArgGlyIleAspValSerProAlaSerAlaAspThrAspVal 197
Db 537 GCGGA-----GCGCGGAGCGGCGATTGGTTCTCCAGCGAGATCACTCCCCGAT--- 487
Qy 198 PheIleAsnIleAspValPheGlyThrIleArgAsnArgThrGluMetHisLeuTyrAsn 217
Db 486 -----CCGTCCCGGTGCGTCTCCACAGC 463
Qy 218 AlaGluThrLeuLysAlaGluThrLysLeuGluTyrPheAlaValAspArgThrAsnLys 237
Db 462 GCCGAGGCTTGACCGCTGCCGATCCAGGAACAGCCGCTGTCGTGTCGTCGCGCATGAG 403
Qy 238 -----LysLeuLeuLys 242
Db 402 CTTGGCGTCCGCTGCAGAGGCCCGACGGCCGAGGCTCAGCATCGTGTGTAAGCGA 343
Qy 243 ProLysThrAsnAlaPheGluAlaAlaTyrLysGluAsnTyrAlaLeuTrpMetGlyPro 262
Db 342 CCGCGCCTTCGCTTTCGCGCTGTCACGCCGATCAC-----GCA 301
Qy 263 TyrLysValSerLysGlyIleLysProThrGluGlyLeuMetValAspPheSerAspIle 282
Db 300 TACCACGTCATGCGCTGCCGACGATCGACAGCCGCTGACACAGCGGCCCGGAGCGTC 241
Qy 283 ArgProTyrGlyAsnHisThr-----GlyAsn 291
Db 240 GAGCGAGCTGGCCCACTCCGCTCCAGAGCTCGTGAAGCCGCCGAATCCGGCGGCCGC 181
Qy 292 SerAlaProSerValGluAlaAspAsnSerHisGluGlyTyrGlyTyrSerAspGlu 310
Db 180 TCGGCGCCACGCGTTTCGACGGGTAGAGGACACGAGGCGCTCGGCGACAGACGAG 124
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Search completed: August 19, 2005, 02:32:36
Job time : 5097 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus.p2n model

Run on: August 18, 2005, 23:14:35 ; Search time 198 Seconds
(without alignment)
2644,488 Million cell updates/sec

Title: US-10-617-835-4

Perfect score: 1645

Sequence: 1 MRARLLIFILSVFILSACG.....SHEGYGSDVAVRQROGOP 320

Scoring table:

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Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-O=/cgn2.1/USPTO.spool.p/US1061735/c/runcat.18082005.115609.8386/app.query.fasta_1.519
-DB=Issued_Patents_NA -QFMT=fastad -SUFFIX=p2n.rnt -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=humand40.cdi
-LIST=45 -DOCALLIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEADSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US1061735 @CGN 1 1.105 @runcat.18082005.115609.8386 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSBLOCK=100 -LONGCLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Issued_Patents_NA:*
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5: /cgn2.6/ptodata/1/ina/ECTUS.COMB.seq:*
6: /cgn2.6/ptodata/1/ina/backfillseq1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1645	100.0	1136	4	US-09-043-302-6
2	1645	100.0	3287	4	US-09-043-302-1
3	106.5	6.5	573	4	US-09-543-681A-268
4	106.5	6.5	1521	4	US-09-489-039A-5599
5	101	6.1	1719	4	US-09-248-796A-1633
6	98.5	6.0	7109	4	US-09-902-540-922
7	97.5	5.9	2196	4	US-09-252-991A-5853
8	97.5	5.9	3036	4	US-09-252-991A-5834
9	97	5.9	1548	4	US-09-489-039A-3464
10	97	5.9	4063	4	US-09-902-540-595
11	95	5.8	1896	4	US-08-426-630-33
12	95	5.8	4748	4	US-08-426-630-29

C 13	95	5.8	4403765	3	US-09-103-840A-2	Sequence 2, Appl1
14	94.5	5.7	1089	3	US-09-071-035-157	Sequence 157, Appl
15	93.5	5.7	1491	4	US-09-252-991A-1243	Sequence 1243, Ap
C 16	93.5	5.7	1551	4	US-09-252-991A-1362	Sequence 1362, Ap
17	93	5.7	2246	4	US-09-252-991A-6782	Sequence 6782, Ap
18	93	5.7	3619	3	US-08-377-503-1	Sequence 1, Appl1
19	93	5.7	3619	3	US-08-177-019-1	Sequence 1, Appl1
20	93	5.7	7152	4	US-09-492-709A-142	Sequence 142, App
21	92.5	5.6	2780	4	US-09-841-786-10	Sequence 10, Appl
22	92.5	5.6	9726	4	US-09-841-786-8	Sequence 8, Appl1
23	92.5	5.6	11130	4	US-09-841-786-15	Sequence 15, Appl
24	92	5.6	3484	4	US-09-949-016-1893	Sequence 1893, Ap
C 25	91.5	5.6	1974	4	US-09-489-039A-6189	Sequence 6189, Ap
26	91.5	5.6	2201	4	US-09-489-039A-5812	Sequence 5812, Ap
27	91	5.5	3600	5	PCT-US95-13749-1	Sequence 1, Appl1
28	91	5.5	15664	1	US-08-402-282-3	Sequence 3, Appl1
29	91	5.5	15664	1	US-08-508-004-3	Sequence 3, Appl1
30	91	5.5	15664	1	US-08-402-066-3	Sequence 3, Appl1
31	91	5.5	15664	1	US-08-402-068-3	Sequence 3, Appl1
32	90	5.5	4308	3	US-08-938-291A-8	Sequence 8, Appl1
33	90	5.5	4308	4	US-09-589-619-8	Sequence 8, Appl1
34	90	5.5	1830121	4	US-09-557-884-1	Sequence 1, Appl1
35	90	5.5	1830121	4	US-09-643-990A-1	Sequence 1, Appl1
36	89	5.4	3687	4	US-09-463-402-1	Sequence 1, Appl1
37	89	5.4	3687	4	US-09-889-572-1	Sequence 1, Appl1
38	89	5.4	3687	4	US-09-117-447-1	Sequence 1, Appl1
39	89	5.4	3768	4	US-09-463-402-12	Sequence 12, Appl
40	89	5.4	4079	4	US-09-016-434-1412	Sequence 1412, Ap
41	89	5.4	4988	4	US-09-463-402-11	Sequence 11, Appl
42	89	5.4	6855	4	US-09-252-991A-6976	Sequence 6976, Ap
C 43	89	5.4	26659	4	US-09-902-540-1237	Sequence 1237, Ap
44	88.5	5.4	1134	4	US-09-540-236-1714	Sequence 1714, Ap
45	88.5	5.4	2643	4	US-09-486-072-6	Sequence 6, Appl1

ALIGNMENTS

RESULT 1
US-09-043-302-6
; Sequence 6, Application US/09043302
; Patent No. 6617128
; GENERAL INFORMATION:
; APPLICANT: MEYER, Thomas F.
; APPLICANT: RUDELI, Thomas
; APPLICANT: SCHUEPPELUG, Ina
; APPLICANT: MAIER, Jurgen
; APPLICANT: EICKERNJAGER, Sandra
; APPLICANT: SCHWAB, Thomas
; TITLE OF INVENTION: Nucleic Acid Molecules Encoding Proteins Which Impact
; TITLE OF INVENTION: the Adhesion of Neisseria Cells to Human Cells
; FILE REFERENCE: 0147-172P
; CURRENT APPLICATION NUMBER: US/09/043.302
; CURRENT FILING DATE: 1998-06-08
; EARLIER APPLICATION NUMBER: PCT/EP96/04092
; EARLIER FILING DATE: 1995-09-18
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 6
; LENGTH: 1136
; TYPE: DNA
; ORGANISM: Neisseria gonorrhoeae
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (135)..(1094)
US-09-043-302-6
Alignment Scores:
Pred. No.: 1,63e-185
Score: 1645.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
DB: 4
Length: 1136
Matches: 320
Conservative: 0
Mismatch: 0
Indels: 0
Gaps: 0

US-10-617-835-4 (1-320) x US-09-043-302-6 (1-1136)

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QY      21 ThrLeuThrGlyIleProSerHisGlyGlyGlyValAspPheAlaValGlnGlnGlnLeu 40
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QY      41 ValAlaAlaSerAlaArgAlaAlaValLysAspMetAspLeuGlnAlaLeuHisGlyArg 60
Db      255 GTGGCCGCTTCGCGCAGAGTCCGCTTAAAGCATGATGATTTTACAGGACATTACAGCAGCA 314
QY      61 LysValAlaLeuTyrIleAlaThrMetGlyAspGlnGlySerGlySerLeuThrGlyGly 80
Db      315 AAAGTTGATGATGATTCATTCGCAATTCATTCGCGCAACGTTTCAGGCACTTTCAGCGGGGT 374
QY      81 ArgTyrSerIleAspAlaLeuIleArgGlyGlyTyrIleAsnSerProAlaValArgThr 100
Db      375 CGCTACTCATTTGATGACCTGATTCGCGGCAATTCATTAACAGCCCTGCGCTCGGCAAC 434
QY      101 AspTyrThrTyrProArgTyrGlyThrThrAlaGlnThrThrSerGlyGlyLeuThrGly 120
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QY      121 LeuThrThrSerLeuSerThrLeuAsnAlaProAlaLeuSerArgThrGlnSerAspGly 140
Db      495 TTAAACCACTCTCTTATTCATCACTTAATGCCCCCTGACCTCGCGCAACCAATCAGACCGT 554
QY      141 SerGlySerArgSerSerLeuGlyLeuAsnIleGlyGlyMetGlyAspTyrArgAsnGly 160
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QY      161 ThrLeuThrThrAsnProArgAspThrAlaPheLeuSerHisLeuValGlnThrValPhe 180
Db      615 ACCTTGACGACCAACCCCGCGACACTGCTTCTTCCCTGCTGCTGCTGCTGCTGCTGCTGCT 674
QY      181 PheLeuAspGlyIleAspValValSerProAlaAsnAlaAspThrAspValPheIleAsn 200
Db      675 TTCCTGCGCGGATTCAGAGCTGTTCTCTCTGCAATGCGCAATCAGATGTTTATTATAC 734
QY      201 IleAspValPheGlyThrIleArgAsnArgThrGluMetHisLeuTyrAsnAlaGlyThr 220
Db      735 ATTCAGCGATTCGGAAGCATTCGCAACGAAACCGAAATGCACTTATACAGCCGAAACA 794
QY      221 LeuLysAlaGlnThrLysLeuGlyLysPheAlaValAspArgThrAsnLysLeuLeu 240
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QY      241 IleLysProLysThrAsnAlaPheGlnAlaAlaTyrLysGlyLysAsnTyrAlaLeuTrpMet 260
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QY      261 GlyProTyrLysValSerLysGlyIleLysProThrGlnGlyLeuMetValAspPheSer 280
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QY      281 AspIleArgProTyrGlyAsnHisThrGlyAsnSerAlaProSerValGlnAlaAspAsn 300
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QY      301 SerHisGlyGlyTyrGlyTyrSerAspGlnAlaValArgGlnHisArgGlnGlyGlnPro 320
Db      1035 AGTCATGAGGGGATTCGATTCAGCATGAGCATGAGCATGAGCATGAGCATGAGCATGAGCAT 1094

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RESULT 2

US-09-043-302-1
Sequence 1, Application US/09043302
Patent No. 6617128
GENERAL INFORMATION:
APPLICANT: MEYER, Thomas F.

```

: APPLICANT: RUDEL, Thomas
: APPLICANT: SCHEUERPLUG, Ina
: APPLICANT: MAIER, Jurgen
: APPLICANT: EICKENRAGER, Sandra
: APPLICANT: SCHWAN, Thomas
: TITLE OF INVENTION: Nucleic Acid Molecules Encoding Proteins Which Impart
: TITLE OF INVENTION: the Adhesion of Neisseria Cells to Human Cells
: FILE REFERENCE: 0147-172P
: CURRENT APPLICATION NUMBER: US/09/043,302
: EARLIER APPLICATION NUMBER: PCT/EP96/04092
: EARLIER FILING DATE: 1998-06-08
: NUMBER OF SEQ ID NOS: 11
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 1
: LENGTH: 3287
: TYPE: DNA
: ORGANISM: Neisseria gonorrhoeae
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (136)..(447)
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (583)..(1542)
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (1585)..(3111)
: US-09-043-302-1
:
: Alignment Scores:
: Pred. No.: 9,45e-185 Length: 3287
: Score: 1645.00 Matches: 320
: Percent Similarity: 100.00% Conservative: 0
: Best Local Similarity: 100.00% Mismatches: 0
: Query Match: 100.00% Indels: 0
: Gaps: 0
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QY      41 ValAlaAlaSerAlaArgAlaAlaValLysAspMetAspLeuGlnAlaLeuHisGlyArg 60
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QY      81 ArgTyrSerIleAspAlaLeuIleArgGlyGlyTyrIleAsnSerProAlaValArgThr 100
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QY      101 AspTyrThrTyrProArgTyrGlyThrThrAlaGlnThrThrSerGlyGlyLeuThrGly 120
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QY      121 LeuThrThrSerLeuSerThrLeuAsnAlaProAlaLeuSerArgThrGlnSerAspGly 140
Db      943 TTAAACCACTCTTATTCATCACTTAATGCCCCCTGACCTTCGCGCAACCATCAGACGCT 1002
QY      141 SerGlySerArgSerSerLeuGlyLeuAsnIleGlyGlyMetGlyAspTyrArgAsnGly 160
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```

Db 1063 ACCTTGACGACCAACCCGCGACACACTGCTTTCTTCCCACTGGTACAGACCGATTT 1122
Qy PheLeuAArgGlyIleAspValValSerProAlaAsnAlaAspThrAspValPheIleAsn 200
Db 1123 TTCCTGCGCGGATAGACGTGTTCTCTCCCAATGCGCATACAGATGTTTATTAC 1182
Qy 201 IleAspValPheGlyThrIleArgAsnArgThrGluMetHisIleuTySerAsnAlaGluThr 220
Db 1183 ATCGACGATTTGCGAACGATACGACAGACAGAACCGAAATGACCTTATACATCCGAAACA 1242
Qy 221 LeuValAlaGlnThrIleLeuGluIuTyPheAlaValAspArgThrAsnIleValLeuLeu 240
Db 1243 CTGAAGACCCCAACAAACTGGAATATTTCCGAGTAGACAGAACCAATTAATAATGCTC 1302
Qy 241 IleValProValThrAsnAlaPheGlyAlaAlaIleValGluAsnTyraIleuThrPhe 260
Db 1303 ATCAAAACCCAAACCAATGCGTTTGAAGCTGCTTAAAGAAATTTACCGCATTTGGATG 1362
Qy 261 GlyProTyrlValSerIleGlyIleValProThrGluGlyLeuMetValAspPheSer 280
Db 1363 GGGCGGATTAAGTAAGCAAGAAATCAACCGAAGGATTAATGTCATTTCTCC 1422
Qy 281 AspIleArgProTyrlGlyAsnHisThrGlyAsnSerAlaProSerValGluAlaAspAsn 300
Db 1423 GATATCCGCGCATACGGCAATCATACGGGTACTCCGCCCCCATCCGTAGAGCTGATAC 1482
Qy 301 SerHisGluGlyIleValSerAspGluAlaValArgGlnHisArgGlnGlyPro 320
Db 1483 AGTCATGAGGGGTATGATACAGCGATGAAAGAGTGGCGCAACATATGACAAAGGACACT 1542

RESULT 3

US-09-543-268
; Sequence 268, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:
; APPLICANT: GARY BRETON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
; FILE REFERENCE: 2709.1002-001
; CURRENT APPLICATION NUMBER: US/09/543,681A
; PRIOR FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/128,706
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO 268
; LENGTH: 573
; TYPE: DNA
; ORGANISM: Proteus mirabilis
US-09-543-681A-268

Alignment Scores:

Pred. No.:	0.00476	Length:	573
Score:	106.50	Matches:	50
Percent Similarity:	40.58%	Conservative:	34
Best Local Similarity:	24.15%	Mismatches:	84
Query Match:	6.47%	Indels:	39
DB:	4	Gaps:	9

US-10-617-835-4 (1-320) x US-09-543-681A-268 (1-573)

Qy 1 MetAlaArgLeuLeuIleProIleLeuPheSerValPheIleuSerAlaCysGly 20
Db 16 CTTAAATAAAGATGTTAAGCTCTATTATACAGTATCTGTTTATACATGACGGT 75
Qy 21 ThrLeuThrGlyIleProSerHisGlyGlyValArgPheAlaValGlnGlnGluLeu 40
Db 76 GTTGCTCTGCGACGACTATGTTAATGTTGTA--ATTAAATTTACTGAGAAAT 132
Qy 41 ValAlaIleSerAlaArgAlaValValValSerMetAspLeuGlnAlaLeuHisGlyArg 60
Db 133 GTTAATGCTGACGTGTTGTTAGTACAAATCAATGATCAAACTGTTAATTTGGCAA 192
Qy 61 LysValAlaLeuTyrlleAlaThrMetGlyAspGlnGlySerGlySerLeuThrGlyGly 80

Db 193 TATGTCACGACCAATTGATAGTGTAGGAAA-----ACAGTGTGT 234
Qy 81 ArgTyrlSerIleAspAlaLeuIleArgGlyIuTyrlIleAsnSerProAlaValArgThr 100
Db 235 AATACTGATTTT-----TATATCAATTTAGAAAGCTGTGATACG 273
Qy 101 AspTyrlThrTyrlProArgTyrlGluThrThrAlaGlnThrThrSerGlyGlyLeuThrGly 120
Db 274 -----ACTGTGACAGAAATGCTTCGTTTCAATTTTCAGT 309
Qy 121 LeuThrThrSerLeuSerThrLeuAsnAlaProAlaLeuSerArgThrGlnSerAspGly 140
Db 310 GTAAGTATTC--AATGATTAATAACATATTAGCTGTAAACAATATTAACAACAGCTGT 366
Qy 141 SerGlySerArgSerSerLeuGlyLeuAsnIleGlyIleMetGlyAspTyrlArgAsnGlu 160
Db 367 GCGGCTGCTGCGACGCGCGTGTGATTAATAAT-----ACAGACCATACAGGAAA 417
Qy 161 ThrLeuThrThrAsnProArgAspThrAlaPheLeuSerHisIleValGlnThrVal--- 179
Db 418 GTGTTA-----CCACAGACGCGCTGTTTCTTCTACAGCAAAACAGTTAATGAT 468
Qy 180 -----PhePheLeuArg-----GlyIleAspValValSerPro 190
Db 469 GATCAATATACACTTAATTTGTTGACGCTTATAATCTAATGATATGATACGTTACCCCT 528
Qy 191 AlaAsnAlaAspThrAspVal 197
Db 529 GGTCACTGCTGATGCTGATGTA 549

RESULT 4

US-09-489-039A-5599
; Sequence 5599, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; PRIOR FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 5599
; LENGTH: 1521
; TYPE: DNA
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-5599

Alignment Scores:

Pred. No.:	0.0239	Length:	1521
Score:	106.50 <td>Matches:</td> <td>60</td>	Matches:	60
Percent Similarity:	37.64% <td>Conservative:</td> <td>39</td>	Conservative:	39
Best Local Similarity:	22.81% <td>Mismatches:</td> <td>85</td>	Mismatches:	85
Query Match:	6.47% <td>Indels:</td> <td>79</td>	Indels:	79
DB:	4	Gaps:	14

US-10-617-835-4 (1-320) x US-09-489-039A-5599 (1-1521)

Qy 9 IleLeuPheSerValPheIleLeuSerAlaCysGlyThr-----Leu 22
Db 769 GTATTAACTGCTGTTATTATTCACATCCTTGTGTGAACCTGTTTTCATACGAAGATTG 828
Qy 23 ThrGlyIleProSer---HisGlyGlyGly---LysArgPheAlaValGlnGlnGluLeu 40
Db 829 AATGGGAACGATGATTCATGCGACAGAAATGAAGAGTGATTTCAACAGCAA--- 885
Qy 41 ValAlaIleSerAlaArgAlaValValValSerMetAspLeuGlnAlaLeuHis---Gly 59
Db 886 -----AAAAAAGATATATATGTCCTCCCTCATCATCATTTGCT 921

Oy 4 ArgIleuaniIeProlIeIeuPheserValPheIleuSerValaCyGslYThrIeuThr 23
 364 CAGCTGGTGGTCCCGGTATGATATGCGGCTTCGCCCTCAAGCCTCCAAAGCCCGCGTGG 423
 Oy 24 Gly-----IleProSerHiGlyGly----- 30
 Db 424 GGCTCGCTGTACGACGCACTCTACGCGACGACGTGATCAGCGAAGAGCGCGCCCGAG 483
 Oy 31 ---GlyIysArgPhe---AlaValGluGlnGluIeuValAlaIleSerAlaArgAlaIle 48
 Db 484 AAAGCGAAAGGCGTCAACACAGATTCGCGGCAAGAGTATCGCTTGCTGGCGGCTTC 543
 Oy 49 ValIysAsp-----MetAspLeuGlnAlaIleuHiIleGly 59
 Db 544 CTCGACGACAGCGCGCGCGCGTGGAGTCCGGCTCCCATGTGCAGCGCAGCTTCACAGCGTG 603
 Oy 60 ArgIysValAlaIeuTyrlIeAlaThrMetGlyAspGlnGlySerGlySerIeuThrGly 79
 Db 604 AAGAAGCGCGCGGTGTGTGTGGCGCTGAAGAACGGCAGCAGAAACCGGCTCGAAGATGCT 663
 Oy 80 GlyArgTyrserrIleAspAlaIeuIleArgGlyGluTyrlIeAsnSerProIaValArg 99
 Db 664 GGCACAGTTC-----CTTGCTTCCAGAGCGACGCGCCGACCGCGAAGCGGTATCTG 714
 Oy 100 ThrAspTyrrThTyrrProArgTyrlGlu-----ThrThrIaGlu 112
 Db 715 CTCAGACGACAAAGCGCTGCACTTGGAAATTCAGATTCAGACCGAGAGCGCGGTGGCCAG 774
 Oy 113 ThrThrSerGlyGlyIeu-----ThrGlyIeuThrThrSerIeuSer 126
 Db 775 ACCGATCCGACGAGCGGTGATGAGACGCTGTGATGAGAGCGCGCTCACCACTCATCTGAGC 834
 Oy 127 ThrIeuAsnAlaProAlaIeuSerArgThrGlnIleAsnAspGlySerGly-SerArgSerSe 146
 Db 835 TGCAGAGAGCTGGTGGCGCG--GGTGCAGCGCGACGACAAAGGTATGATCTTACCGACATG 893
 Oy 146 rIeuGlyIeuAsnIleGlyGlyMetGlyAspTyrrArgAsnIu-----Th 161
 Db 894 GCTGGGGCTGTGAAAGGCGACCTGGCGGAGGAAGTACGACAAAGGCGGAGCAGCACTTCAC 953
 Oy 161 rIeuThrThrAsnPro-----ArgAspThrAlaPheIeuSerHiIle 175
 Db 954 CCGCAGCATGTAACCCGAGCCGCGTCTACACCAAGGCGCAGCGGTTCGACATGACCTCGCA 1013
 Oy 175 uValGlnThrValPhePheIeuArgGlyIleAspValValSerProIeAsnAlaAspTh 195
 Db 1014 CGGCGGCTCGCTGCTTTCGTGGCGACAGTGGCGACCTGATGACCAAGATGCCATCTT 1077

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QY      195 AspyalPheileAsnIleaspVal-----PheGlyThrIleArgSnaR 210
           |||          :|||          :|||
Db      1074 CGACAAGACGGCAAC--GAAGTCGGAAAGCATCCAGACGCTGTACCACGCT 1130
QY      210 gThrglumeChisLeuTYrAenAlagluThrLeuylSaIagInThrylsLeugluTyPh 230
           ::|||       |||         |||
Db      1131 GATGCCATTCTATGACTCGAAGCGGCACACCGACCGCAGAAGAACGC----- 1176
QY      230 eaIaVaIaspaIrghThraSnlyslvsLeuLeuIlysProIysThrsAnaIaPhegluaI 250
           |||         |||         |||
Db      1177 -----CGCACCGGCACGCGTGTATATGCTCAAGCCGAAGATGACGCGTCCGGAAGA 1226
QY      250 aaIaTyrlrysGluslnTYrAlaleuTrpmecGlyProtyrlrysValserlysglyIely 270
           |||         |||         |||
Db      1227 AGCGCCCTTCACCAACGA-GCT-----GTTG 1252
QY      270 sProthrGlnGlyLeuMecValaAspPheSerAspIleaRgProtyrlGlysnHsthrGI 290
           |::|        :|||         |||
Db      1253 GCCGGTGTAAGAGACGCTCTCGCGCTCGCGCCGCAA---CACCTTAAGTCCGCAATATGG 1309
QY      290 yAsnsErAlaPro---SerValGluAlaAspASerHisgluGlyTyrlGlyTyrsEras 309
           |||         |||         |||
Db      1310 ACGAGAGACGCGGCACACACCGTGAACTGGAAGCGCTGCATCAAGGC---GGCCAAGATC 1366
QY      309 pGluAlaValaIargGlnHtsarGlngInglnPro 320
           |||         |||         |||
Db      1367 GCGTGGTGTTCATCAACACCGGCTTCCTCCACGC 1400

RESULT 8
US-09-252-991A-5934/C
; Sequence 5934, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 5934
; LENGTH: 3036
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-5934

Alignment Scores:
Pred. No.:      0.88      Length:      3036
Score:          97.50     Matches:      83
Percent Similarity: 37.63% Conservative: 57
Best Local Similarity: 22.31% Mismatches: 152
Query Match:      5.93%   Indels:      82
DB:               4       Gaps:      16

US-10-617-835-4 (1-320) x US-09-252-991A-5934 (1-3036)
QY      4 ArgIeuLeuIleProIleLeuPheSerValPheIleuSerAlaCySglyThrLeuThr 23
           |||         |||         |||
Db      1941 CAGCTGGGtggGgcGGGTATGATGCGGCTTCGCCCTCAACGCTCCCAAGCCCGCTGG 1882
QY      24 Gly-----IleProSerHisglyGly----- 30
           |||         |||         |||
Db      1881 GGCTTCGCTTACGACGCACTTACGGCACCGACGCTGATCAAGCAAGAGCGGCGCGAG 1822
QY      31 ---GlyIysArGphe---AlaValGluGlnGluLeuValAlaIasEraIaArgValaLa 48
           |||         |||         |||
Db      1821 AAAGGCAAGGGGCTACACACAGAGTTTCGGGCGACAAAGTTCATCGCTTCGCGGCTTC 1762
QY      49 ValIysAsp-----MetAspLeuGlnAlaIeunHisGly 59

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Db 1761 CTCGACGAGGCGCCCGCTGGAGTCCGGCTCCCATGTCTGACGCCACTTCTTACAGCCGTG 1702
::: :::
QY ArgValValAlaLeuThrIleAlaTherMetGlyAspGlnGlySerGlySerLeuThrGly 79
::: ||||| ::::|
Db 1701 AAGAACGGCGCGCTGTGCTGTGCGCTGAAAGAACGGCAGCGCAAGCGCTTGAAGATGCT 1642
80 GlyAlaGlySerIleAspAlaLeuIleArgGlyGlyThrIleAsnSerProAlaValArg 99
1641 GCCCAGTTTC-----CTTGCCTTCAGGCGCAGCGCCGCAAGCCGCAAGCGGTACTG 1591
QY ThrAspGlyThrThrProArgTyrglu-----ThrThralaglu 112
1590 CTCGAGCCAAACGCGCTGCACCTTCCAAATCCAGATCGACCCGACGAGCCCGGTGCGCAG 1531
QY ThrThrSerGlyGlyLeu-----ThrglyLeuThrThrSerLeuSer 126
1530 ACCGATGCGCGCGAGGGGTGAAGAGAGCGTGTGATGAGAACGCGCCTCACCACCATCATGAGAC 1471
Db 127 ThrLeuAsnAlaProAlaLeuSerArgThrGlnSerAspGlySerGly-SerArgSer 146
1470 TCGCAGGACCTGGTGTCGCGC--GGTGGAGCGCGACACCAAGGTAGTATCTTACCGACATG 1412
QY rleuglyLeuAsnIleGlyGlyMetGlyAspPtyrArgAsnIle-----Th 161
1411 GCTGGGCGCTGATGAAGCGAGCATGTGCCGAGAGATCAGCAAGGGCGGACGACCTTCC 1352
Db 161 rleuThrThrAsnPro-----ArgAspThrAlaPheLeuSerHisle 175
1351 CCGCAGCATTGAACCGCGAGCCGGTCTACACAGAGCGCGACGGTTCGAACTGACCTGCA 1292
QY 175 vvalGlnThrValPhePheLeuArgGlyIleAspValValSerProAlaAsnAlaAspTh 195
1291 CGCGCGCTGCGCTGTTGTTGTCGCGCAACGTGCGCCACCTGATGACCAACGATGCGATCTCT 1232
QY rAspValPheIleAsnIleAspVal-----PheGlyThrIleArgAsnAr 210
1231 CGACAGGACGGGCAAC--GAAGTCCGGAAAGCATCCAGACGGGTCTGTTACCAAGCTT 1175
Db 210 gThrGlnMetHisLeuTyrrAsnAlaGluThrLeuLysAlaGlnThrIleGluIuTyrrh 230
1174 GATGCCATTCTATGACCTGAACCGCAACACGACCGCGCAAGAACAC----- 1129
QY 230 eAlaValAspArgThrAsnLysLysLeuLeuIleLysProLysThrAsnAlaPheGluAl 250
1128 -----CGCACCGCGACGCTGATATGCTCAAGCGCGAAGACGAGTCCGGAAGA 1079
QY aAlaTyrrLysGluAsnTyrrAlaLeuThrMetGlyProTyrrLysValSerLysGlyIleL 270
1078 AGCGCGCTTCCACCAACGA-GCT-----GTTCTG 1053
Db 270 sProThrGlnGlyLeuMetValAspPheSerAspIleArgProTyrrGlyAsnHisThrG 290
1052 GCCCGGTGAGAGACGTCTCGGCTCGCGCGCGA---CACCTTGAAGTCCGCAATCATGG 996
QY yAsnSerAlaPro--SerValGluAlaAspAsnSerHisGlnGlyTyrrGlyTyrrSerAs 309
995 ACGAGAGACGCGCGACACCGTGAACCTGAAGCTGCATCAAGGC---GGCCAAAGATC 939
Db 309 pGluAlaValArgGlnHisArgGlnGlyGlnPro 320
938 GCGTGTGTTTCATCAACACGCGCTTCTTCGACCG 905

RESULT 9
US-09-489-039A-3464
; Sequence 3464, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489.039A

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; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 3464
; LENGTH: 1548
; TYPE: DNA
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-3464

Alignment Scores:
Pred. No.: 0.331 Length: 1548
Score: 97.00 Matches: 60
Percent Similarity: 34.93% Conservative: 42
Best Local Similarity: 20.55% Mismatches: 130
Query Match: 5.90% Indels: 60
DB: 4 Gaps: 10

US-10-617-835-4 (1-320) x US-09-489-039A-3464 (1-1548)
QY 73 GlySerGlySerLeuThrGlyGlyArgTYrSerIleAspAlaLeuIleArg----- 89
DB 433 GGGGCTGGGAGATTTCACTCCAGCGCTTTAGTAAATACATATGTGAGATTAATACAA 492
QY 90 -----GlyGlyTrpIleAsnSerProAla----- 97
DB 493 CCATCCCTTGGCAATTAATTCAGAACCTCGCATCGAAGAGTGCGTTTCTAGTCTCT 552
QY 98 -----ValArgThrAspTYrThrTYrProArgTYrGluThr----- 110
DB 553 GCTGATAGCTTCAATTCGAATAATATTCACATAAAGATATCAATCAACCTCCAAA 612
QY 111 -----AlaGluThrThrSerGlyLeuThrGlyLeuThrThrSerLeu 125
DB 613 TATCAAGGTAGTAAGTAAGAAAGAAATACCTCGCATTTGCTTGATGATCTTTTAA 672
QY 126 SerThrLeuAsnAla-----ProIleLeuSerArg 135
DB 673 CATCGTTTAGACCAATTAATTAATGATGATGCCCTAAGTACGACGCGGAAATGG 732
QY 136 ThrGlnSerAspGlySerGlySerArgSerSerLeuGlyLeuAsnIleGlyGlyMetGly 155
DB 733 GATTAAGCTGAGCTATTCGATGACCAACCTCCCTTGATGACAAAGCCGGGACAGCGT 792
QY 156 AspTYrArgAsnGluThrLeuThrThrAsnPro--ArgAspThrAlaPheLeuSerHis 174
DB 793 CCTTGGCGAGCATATTCATTTCTTAATACAAATAAACAACCTTTTGGCAGCAT 852
QY 175 LeuValGlnThrValPhePheLeuArgGlyIleAspValIleSerProIleAsnAlaAsp 194
DB 853 ATTTATCTGGGCGCTTAGGCGTGGTGGGCGAGCTGTAGTGTGGCAAGATAACGTACTA 912
QY 195 ThrAspValPheIleAsnIleAspValPheGlyThrIleArgAsnArgThrGluMetHis 214
DB 913 TTTAGAGCTGGGTGTGACGAGATGTCCCGCGATTAATGATGAATAAGTAACTCCAT 972
QY 215 LeuTYrAsnAlaGluThrLeuGlyAlaGlnThrLysLeuGluTYrPheAlaValaAspArg 234
DB 973 -----ACCATCTTGCGCTTACCAACTGATCTTTTACCACCATGCGCTAAA 1020
QY 235 ThrAsnLysLysLeuLeuIleLysProLysThrAsnAlaPheGluAlaIleTYrLysGlu 254
DB 1021 ACCAAT-----GATTTGTTTTTCACTAAAGGAGCGCAAAAACAATAATACAGCAAGA 1074
QY 255 AsnTYrAla-----LeuTYrMetGlyProTYrLysValSerLysGlyIleLysProThr 272
DB 1075 AACTGATACGAGAAATGTTGGGATACAGACCTGCGTAACAAT----- 1116
QY 273 GluGlyLeuMetValAspPheSerAspIleArgProTYrGlyAsnHisThrGlyAsnSer 292
DB 1117 -----ATGCTTAGTTTGGTAAAGCGACACCTTGTGATGATCCGACATTTGGGTTT 1167
QY 293 AlaProSerValGluIleAspAsnSerHisGluGly-----TYrGlyTYr 307

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DB 1168 GCGCCACAAAGACTTTGGCACAAGCCACACCTCGGCGCATTTGAAAAGTATGATGAC 1227
QY 308 SerAspGluAlaValArgGlnHisArgGlnGlyGln 319
DB 1228 AACCTGAAAGAAACGACAAAGCGTACTGAAGGTGA 1263

RESULT 10
US-09-902-540-595/c
; Sequence 595, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 595
; LENGTH: 4063
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-595

Alignment Scores:
Pred. No.: 1.63 Length: 4063
Score: 97.00 Matches: 78
Percent Similarity: 35.36% Conservative: 50
Best Local Similarity: 21.55% Mismatches: 120
Query Match: 5.90% Indels: 114
DB: 4 Gaps: 15

US-10-617-835-4 (1-320) x US-09-902-540-595 (1-4063)
QY 1 MetArgAla--ArgLeuLeuIleProIleLeuPheSerValPheIleLeuSerAlaCys 19
DB 2940 ATGCGGCGCCATCAGCGCCCTGCTCCCATCTC-----GCCCTGCTGACCGCATGT 2887
QY 20 GlyThrLeuThrGlyIleProSerHisGlyGlyLysArgPheAlaValGluGlnGly 39
DB 2886 TCTGATCCGCGCCTCCCGCAGTACGAGACTGACCGGACGTGCGCATCACACGAGAG 2827
QY 40 LeuValAlaIleSerAlaArgAlaValLysAspMetAspLeuGlnAlaLeuHisGly 59
DB 2826 GCGCTCGCGCGCATCTCGCGCAGGCTTATCGCACTCCCTCACCGCTTCGGAGGC 2767
QY 60 Arg-----LysValAla-----LeuTYrIleAla 67
DB 2766 ACGCGTCTATTGCGGCGCTCGCGCAGGCGGACACTCCACCGGATCAGACTCTCC 2707
QY 68 ThrMetGlyAspGlnGlySerGlySerLeuThrGlyArgTYrSerIleAspAlaLeu 87
DB 2706 ACCCTGGGGAATACACCGGAGCGCCCAATGCGCAGGACCTCATCTTGCACGCGGAG 2647
QY 88 IleArg----- 89
DB 2646 GTCCGTGATCCCGGAGCGAGACTGTGCGCGCACAGTTCGAGCTCGAGTCTCAAGCC 2587
QY 90 GlyGlyTrpIleAsnSerProAlaValArgThrAspTYrThrTYrProArgTYrGluThr 109
DB 2586 GCGCTCGAGTGGCGCTCATCCAGCTCCCGATGATACGTGCGGACAACTACGCGCG 2527
QY 110 ThrAlaGluThrThrSerGlyGlyLeuThrGlyLeuThrThrSerLeuSerThrLeuAsn 129
DB 2526 CAACTGAT--GCTTCGGGCGGACAGCGCGTACACTGACGCTCGGAGGGGACCC 2470
QY 130 AlaProAlaLeuSerArgThrGlnSerAspGlySerGlySerArgSerSerLeuGlyLeu 149

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Db 2469 CTCGGCTGGGGCTGCGCTCGATACACAGGG----- 2437
Qy 150 AsnIleGlyGlyMetGlyAspIlyrArgAsnGluThrLeuThrAsnProArgAspThr 169
Db 2436 CACATCTCGGGGT----- 2422
Qy 170 AlaPheLeuSerHisLeuValGlnThrValPhePheLeuArgGlyIleAspValValSer 189
Db 2422 ----- 2422
Qy 190 ProAlaAsnAlaAspThrAspValPheIleAsnIleAspValPheGlyThrIleArgAsn 209
Db 2421 CCGCGCACCTCGGACCC-----TTCTCCGTCACCGTC----- 2389
Qy 210 ArgThrGluMetHisLeuThrAsnAlaGluThrLeuGlyAspAlaGlnThrIleGluGlu--- 228
Db 2388 -----CACGTGAGAGACCGCACCGGGCTTTGAGACCAAGTGTCTTCGCTC 2341
Qy 229 -----TyrPheAlaValAspArgThrAsnIlyValLeuLeuIleIlyS 242
Db 2340 TCCACTTTCACCGGCGCTATCTCGCAGCGACAGCTC----- 2302
Qy 243 ProIlyThrAsnAlaPheGluAlaAlaIlyrIlyGluAsnIlyrAlaLeuTrpMetGlyPro 262
Db 2301 CCTCCCGCTCGCTCGAGCGCTTCTCACTCCAGAGCTTCCGCGGAGGCGGACCA 2242
Qy 263 -----TyrIleValSerIlyGlyIleIlySProThrGluGlyLeuMetValAspPhe 279
Db 2241 CCGCTACGTTCCGATACCTCAGGTGCTTCCGACG--GGCTTCAACTGATGCC 2185
Qy 280 SerAspIleArgProIlyrGlyAsnHisThrGlyAsnSerAlaProSerValGluAlaAsp 299
Db 2184 AGCGGTGTCGAGGACACCGACGACGAGCGCGCTCTTCAAGTGAATCCAG 2125
Qy 300 AsnSerHisGluGlyIlyrGlyIlyrSerAspGluAla--ValArgGlnHisArgGlnIlyG 319
Db 2124 GAGCGCAAT-----GGCGGTGCTGTCGCGCACGTTCAACTCAGCTCCAGGAGC 2074
Qy 319 In 319
Db 2073 GG 2072

RESULT 11
US-08-426-630-33/c
; Sequence 33, Application US/08426630
; Patent No. 6656709
; GENERAL INFORMATION:
; APPLICANT: BLANCHE, FRANCIS, CAMERON, BEATRICE, CROUZET,
; APPLICANT: JOEL, DEBUSCHE, LAURENT, LEVY SCHIL, SOPHIE,
; APPLICANT: THIABAUT, DENIS
; TITLE OF INVENTION: POLYPEPTIDES INVOLVED IN THE
; TITLE OF INVENTION: BIOSYNTHESIS OF COBLAMINS AND/OR COBAMIDES, DNA SEQUENCES
; TITLE OF INVENTION: CODING FOR THESE POLYPEPTIDES, PREPARATION METHOD AND THEIR
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN
; STREET: 555 13TH STREET, N.W.
; CITY: WASHINGTON
; STATE: DISTRICT OF COLUMBIA
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/426,630
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/916,151

; FILING DATE: 14-SEP-1992
; APPLICATION NUMBER: PCT/FR91/00054
; FILING DATE: 30-JAN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: F. F. CALVERT
; REGISTRATION NUMBER: 28,557
; REFERENCE/DOCKET NUMBER: 1290-7213
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 857-7887
; TELEFAX: (202) 857-7929
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1896 base pairs
; TYPE: Nucleic acid
; STRANDEDNESS: Double
; TOPOLOGY: Unknown
; MOLECULE TYPE: cDNA
; HYPOTHEICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Pseudomonas dentrificans
; STRAIN:
; INDIVIDUAL ISOLATE:
; DEVELOPMENTAL STAGE:
; HAPLOTYPE:
; TISSUE TYPE:
; CELL TYPE:
; CELL LINE:
; ORGANELLE:
; FEATURE:
; NAME/KEY: COBT
; LOCATION: 2616-4511 bp of SEQ ID NO: 29
; IDENTIFICATION METHOD:
; OTHER INFORMATION:
; US-08-426-630-33

Alignment Scores:
Pred. No.: 0.801 Length: 1896
Score: 95.00 Matches: 73
Percent Similarity: 31.10% Conservative: 34
Best Local Similarity: 21.22% Mismatches: 99
Query Match: 5.78% Indels: 138
DB: 4 Gaps: 17

US-10-617-835-4 (1-320) x US-08-426-630-33 (1-1896)

Qy 14 PheIleuSerAlaCySGlyThrLeuThrGlyIleProSerHisGlyGlyIlyAspArg 33
Db 1854 TTCTCTCTCGAAGAGTGGGCGACCTGTCGT-----CATCGCGCGGCAAGCTC 1804
Qy 34 PheAlaValGluGln---GluLeuValAlaAlaSerAlaArgAlaValIlyAspMet 52
Db 1803 ATCGGATCGACGATGTGACGCGACGCGCATGAGCGCTCACGTGCGCGCATACC 1744
Qy 53 AspLeuGlnAlaLeuHisGlyArg-----LysVal 62
Db 1743 GATCGCGACGATTCACCGCGGCGGCTTTCATCTGCTCATGACCGCGCGAGGTG 1684
Qy 63 AlaLeuThrIleAlaThrMetGlyAspGlnIlySerGlySerLeuThrGlyIlyArgTyr 82
Db 1683 ACGCTCCAGATGTTCTCTGATTGACGA-----CACGTTGCA 1645
Qy 83 SerIleAsp--AlaLeuIleArgGlyIlyThrIleAsnSerProAla----- 97
Db 1644 GTCTGACCGCGCGCGCGCTCCGAATCATCATCATGATGCGCGCTTTCGCGCGCGC 1585
Qy 98 -----ValArgThrAspTyrThr 103
Db 1584 CATGACCGCTCATGCGCGCCCAATCAACGCTGCGCGCTCATGATGTTTCTTGACAGAGCC 1525
Qy 104 TyrProArgIlyrGluThr----- 109
Db 1524 TTCCCGCATCATCAGCGCGAGATTGCGTGTGCGCGCGCGCACGAGCGTCCGACACTT 1465

```

QY 110 -----ThralagluThrThrseryl----- 116
Db 1464 GTAGACATGTGTCCAGAGTCTTAAAGCGACCCGGGCTGTGCTGCTGCCCGCCGAC 1405
QY 117 -----GlyLeuThnGlyLeuThrThrseryl 126
Db 1404 CCACTTCGCGTACGTCGCCACCTTCACAGCCTTGGTGTAACAGAGATCTCAC 1345
QY 127 ThrLeuAmlAProAlaLeuSerArgThrglnSerAap-----GlySerGlySer 143
Db 1344 ---CTTGACGCCCGCGCTGACGCTGCGCGCCAGATATCGCGCGAGTGTGCGCGAAC 1288
QY 144 ArgSerSerLeuGlyLeuAmlleGlyGlyMetGlyAap---TyrArgAmlGlnThre 162
Db 1287 CGTATCGGACGCGCGCGCATGACCGGAAATTTGTCATCAGACGCTACACGATATC 1228
QY 163 ThrThraenProArgAapThraLapheLeuSerHisLeuValGlnThraValPhePhe 182
Db 1227 GCGGAA-----GTTGGTGTCTTTCGCGCTT 1201
QY 183 ArgGly-----IleAapValValSerProAlaAmlAapThr 195
Db 1200 GAAGGAAAGCGGCTCATCGATCATGATGATGCGTGAAGCCCGCGCATCGAGATA 1141
QY 196 AapValPheIleAmlleAapValPheGlyThrIleArgAmlArgThrgluMetHis 215
Db 1140 CCCCTCTC-----GAGATCGAATC 1120
QY 216 TyrAmlAgluThrLeuValleGlnThryleGluTyrPhe-----AlaValAap 233
Db 1119 CCAGAGGCGGTTCCTGCTGCGCATCAGCGCGCTGCGAGCGGTTGGCAGCGCGCAC 1060
QY 234 ArgThraenLysLeuLeuLysProLysThraAmlAapheGluAlaTyrLys 253
Db 1059 CGC----- 1057
QY 254 GluAmlTyrAlaLeuTyrMetGlyProTyrLysValSerLysGlyLysProThrglu 273
Db 1056 -----GCCTTGAAGATGGGCAAGCTGCTTTCAGAGAGGCGCGCGGCTGCA 1006
QY 274 ---GlyLeuMet 276
Db 1005 CTCGCGCTCGTC 994

RESULT 12
US-08-426-630-29/c
; Sequence 29, Application US/08426630
; Patent No. 6656709
; GENERAL INFORMATION:
; APPLICANT: BLANCHE, FRANCIS; CAMERON, BEATRICE; CROUZET,
; APPLICANT: JOEL; DEBOSCH, LAURENT; LEVEY SCHIL, SOPHIE;
; TITLE OF INVENTION: POLYPEPTIDES INVOLVED IN THE
; TITLE OF INVENTION: BIOSYNTHESIS OF COBALAMINS AND/OR COBAMIDES, DNA SEQUENCES
; TITLE OF INVENTION: CODING FOR THESE POLYPEPTIDES, PREPARATION METHOD AND THEIR
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & PINNEGAN
; STREET: 555 13TH STREET, N.W.
; CITY: WASHINGTON
; STATE: DISTRICT OF COLUMBIA
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/426,630
; FILING DATE:
; CLASSIFICATION: 435

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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/916,151
; FILING DATE: 14-SEP-1992
; APPLICATION NUMBER: PCT/FR91/00054
; FILING DATE: 30-JAN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: F. F. CALVETTI
; REGISTRATION NUMBER: 28,557
; REFERENCE/DOCKET NUMBER: 1290-7213
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 857-7887
; TELEFAX: (202) 857-7929
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4748 base pairs
; TYPE: Nucleic Acid
; STRANDEDNESS: Double
; TOPOLOGY: Unknown
; MOLECULE TYPE: CDNA
; HYPOTHETICAL: No
; ORIGINAL SOURCE:
; ORGANISM: Pseudomonas denitrificans
; STRAIN:
; INDIVIDUAL ISOLATE:
; DEVELOPMENTAL STAGE:
; HAPLOTYPE:
; TISSUE TYPE:
; CELL TYPE:
; CELL LINE:
; ORGANELLES:
; FEATURE:
; NAME/KEY:
; LOCATION:
; IDENTIFICATION METHOD:
; OTHER INFORMATION: Nucleotide sequence of the 5' to 3'
; Patent No. 6656709
; OTHER INFORMATION: strand from the 4748 bp SalI-SalI-SalI-SalI-BglI fragmen
; US-08-426-630-29
; OTHER INFORMATION: Pseudomonas denitrificans

Alignment Scores:
Pred. No.: 3.65 Length: 4748
Score: 95.00 Matches: 73
Percent Similarity: 31.10% Conserves: 34
Best Local Similarity: 21.22% Mismatches: 99
Query Match: 5.78% Indels: 138
DB: 4 Gaps: 17

US-10-617-835-4 (1-320) x US-08-426-630-29 (1-4748)
QY 14 PheIleLeuSerAlaCyeGlyThrleuThrglyleProserHisGlyGlyLysArg 33
Db 4469 TTCGCTCCGAAGAGTGGCGGCGAGCTGTCGCT-----CATCGCGCGCAAGCTC 4419
QY 34 PheAlaValGluGln---GluLeuValAlaAlaSerAlaArgAlaAlaValLysApmec 52
Db 4418 ATCGCATCGACGATGTGACGCGACGCGATAGTACGCGGTACGCTGCGCATACC 4359
QY 53 AapLeuGlnAlaLeuHisGlyArg-----LysVal 62
Db 4358 GATCGCGCAGAGTTCACCGCGCGCGCTTTCATCTGTCGATGACCGCGCGAGGTG 4299
QY 63 AlaLeuTyrIleAlaThrmecGlyAapGlnLysSerGlySerLeuThrglyGlyArgTyr 82
Db 4298 ACGCTCCAGATGTTCTCTGATTCACGA-----CAGCGTGA 4260
QY 83 SerIleAap---AlaLeuIleArgGlyGluTyrIleAmlSerProAla----- 97
Db 4259 GTCTGCACCGCGCGCGCGCTCGAAATCATATCATAGATGCGCGCTTTCGCGCGCGC 4200
QY 98 -----ValArgThraApyTyrThr 103
Db 4199 CATGACCGCTCATGCGCCCAATCAACGCTCGCGCTGATGTTTCTTTCGAGCAGGCC 4140

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Qy 104 TyrProArgTyrGluThr----- 109
   |||
Db 4139 TTCCTCCATCATCAGCGGAGATTGCTGTCGCGCCGCGCCACGAGCTCGGACAGCTT 4080
Qy 110 -----ThrAlaGluThrSerGly----- 116
   |||
Db 4079 GTACAGCATGTGTGCGAGGTCGTTGAGGCAACCGCGGGCGTGTGCTTCCGCGGCGAG 4020
Qy 117 -----GlyLeuThrGlyLeuThrThrSerLeuSer 126
   |||
Db 4019 CCACTTCGCGGTACGTCGCCACCTTCACGCTTGCTGTAAACCGAGGATCTTCAC 3960
Qy 127 ThrLeuSnaIProAlaLeuSerArgThrGlnSerAsp-----GlySerGlySer 143
   |||
Db 3959 ---CTTACGCCCGAGCGCTCGAGCGTCGCCGCGGAGATACCGCGCGAGTGGCGGCAAC 3903
Qy 144 ArgSerSerLeuGlyLeuAsnIleGlyGlyMetGlyAsp---TyrArgSnaIuThrLeu 162
   |||
Db 3902 CGTGATCGGACGCGCGCGCATGAGCGGAATTGTCATCAGACGCTCACGACGCGTATC 3843
Qy 163 ThrThrAsnProArgAspThrAlaPheLeuSerHisLeuValGlnThrValPhePheLeu 182
   |||
Db 3842 GCGGAA-----GTTGGTCTCTTTTCGCGCTT 3816
Qy 183 ArgGly-----IleAspValValSerProAlaAsnAlaAspThr 195
   |||
Db 3815 GAAGGAAGCGCGCTGCATCGGATCGATGATGATCGCTGAAGCCGCGCGGATCGAGATA 3756
Qy 196 AspValPheIleAsnIleAspValPheGlyThrIleArgAsnArgThrGluMetHisLeu 215
   |||
Db 3755 CCCCTCTTC-----GAGATCGAACTC 3735
Qy 216 TyrAsnAlaGluThrLeuValAlaGlnThrIleGluIuThrPhe-----AlaValAsp 233
   |||
Db 3734 CCAGAGCGGCTTCGCTGCGCATCAGCGCGCGCTGACGCGGTTGGCAAGCGCGCAC 3675
Qy 234 ArgThrAsnIleValLeuLeuIleLeuPheProIleThrAsnAlaPheGluAlaIleValLeu 253
   |||
Db 3674 CGC----- 3672
Qy 254 GluAsnTyrAlaLeuTyrMetGlyProTyrIleValSerIleGlyIleLeuPheProThrGlu 273
   |||
Db 3671 -----GCCTTGAGATGGGCAAGCTGCTTCGAGGAAGCGCGCACGCGTGCAG 3621
Qy 274 ---GlyLeuMet 276
   |||
Db 3620 CTCGACCTCTGC 3609

RESULT 13
US-09-103-840A-2/c
; Sequence 2, Application US/09103840A
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103.840A
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 4403765
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; FEATURE:
; OTHER INFORMATION: CDC 1551
; OTHER INFORMATION: "n" bases at various positions throughout the sequence
; OTHER INFORMATION: represent a, t, c or g
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US-09-103-840A-2
Alignment Scores:
Pred. No.: 2 74e+05 Length: 4403765
Score: 95.00 Matches: 50
Percent Similarity: 36.68% Conservative: 23
Best Local Similarity: 25.13% Mismatches: 76
Query Match: 5.78% Indels: 50
DB: 3 Gaps: 10

US-10-617-835-4 (1-320) x US-09-103-840A-2 (1-4403765)
Qy 105 ProArgTyrGluThrThrAlaGluThrThrSerGlyLeuThrGlyLeuThrThrSer 124
   |||
Db 315896 CCTGAGCTGGAGGAAGACGATGACAACA----- 315867
Qy 125 LeuSerThrLeuSnaIProAlaLeuSerArgThrGlnSerAspGlySerGlySerArg 144
   |||
Db 315866 CTGGAAATCTGCGCAGCGGACCGGCTGCTCGAAGACCTCGGCGCTGCGGAGCTG 315807
Qy 145 SerSerLeuGlyLeuAsnIleGlyGlyMetGlyAspTyrArgAsnGluThr----- 161
   |||
Db 315806 GCCATCTCGGTGTGTCGTCGATCGGTCGCGGCGGACCGCGCTCCACAGCTGGCCAC 315747
Qy 162 ---LeuThrThrAsnProArgAspThrAlaPheLeuSerHisLeuValGlnThrValPhe 180
   |||
Db 315746 CGGCTAGTCGCGCAACCCGACGATGGGC-----ACGTCGAAGTGACCTTC 315699
Qy 181 -----PheLeuArgGlyIleAspVal---ValSerProAlaAsnAlaAsp 194
   |||
Db 315698 GCGGCTTCGCGCGCGGCTTCGCGGCGGACGCTCAACATCGCGGTGAGCGGCGGAC 315639
Qy 195 ThrAspValPheIleAsnIleAspValPheGlyThrIleArgAsnArgThrGluMetHis 214
   |||
Db 315638 ACCGATCCGACCGCGGAAGGATGATGTCGACCC-----AACAGATTCACAC 315588
Qy 215 LeuTyrAsnAlaGluThrLeuValAlaGlnThrIle-----LeuGluThrPhe 230
   |||
Db 315587 GTCCGGAGCGGCCGATGATCTCACTGGGACCCGCGCGCGGCTGCGGACCTATCTG 315528
Qy 231 AlaValAspArgThrAsnIleValLeuLeuIleLeuPheProIleThrAsnAlaPheGluAla 250
   |||
Db 315527 GCGGTG-----CGCGGCGCGCTGTGTGAGGCC----- 315498
Qy 251 AlaTyrIleGluAsnTyrAlaLeuTyrMetGlyProTyrIleValSerIleGlyIleValLeu 270
   |||
Db 315497 -----GTGCTGGGTCAAGCAGCTACGACGTCGATGTCGCGCATCGGC 315456
Qy 271 ProThrGluGlyLeuMetValAspPheSerAspIleArgProTyrGlyAsnHisThr 289
   |||
Db 315455 CCGTCGCGC-----CTACGCGCGGAGACGTCGTCGCGGCGGAGACACAC 315408

RESULT 14
US-09-071-035-157
; Sequence 157, Application US/09071035
; GENERAL INFORMATION:
; APPLICANT: GIL H. Choi
; TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides
; CORRESPONDENCE ADDRESS: 496
; ADDRESS: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
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APPLICATION NUMBER: US/09/071,035
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: A. Anders Brookes
 REGISTRATION NUMBER: 36,373
 REFERENCE/DOCKET NUMBER: PB369P2
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (301) 309-8504
 TELEFAX: (301) 309-8512
 INFORMATION FOR SEQ ID NO: 157:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1089 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 US-09-071-035-157

Alignment Scores:
 Pred. No.: 0.368 Length: 1089
 Score: 94.50 Matches: 53
 Percent Similarity: 38.43% Conservatve: 30
 Best Local Similarity: 24.54% Mismatches: 96
 Query Match: 5.74% Indels: 37
 Gaps: 10

US-10-617-835-4 (1-320) x US-09-071-035-157 (1-1089)

QY 10 LeuPheSerValPheIleuSerAlaCys-----GlyThrLeuThrGlyIlePro 26
 |||||
 DB 100 TTATTAGGTAACAACTTTAGCGGCTGTGGAGCGCGGAACGTCAATGCTCAAC 159
 27 SerHieGlyGlyIleYs-----ArgPheAlaValGluGlu 39
 ::::|
 DB 160 GCGTGTGGGCGGTAAGGCAAGTGGCAAGTTTTCGTCTCAGACAGACAGACAG 219
 40 LeuValAlaIleSerAlaArgAlaValIleYsPheMetAspLeuGlnIleuHieGly 59
 ::::|
 DB 220 ATGCCAACAGCTGATTTATCACTAGCAGACAGACAGATTAAGTTTATTCGATTAATAAT 279
 60 ArgIleValAlaLeuTyrlleAlaThrMetGlyAsp-----GlnGlySerGlySerIleu 77
 ::::|
 DB 280 GTATATGAAGAAATTTATGTTTAAACAAGATTAACAAAGTCCAACTGCGAGTGCAGCG 339
 78 ThrGlyGlyArgTySerIleAspAlaLeuIleArgGlyGlyIleu----- 94
 |||||
 DB 340 GAAAAAGCAAGTTTCTGAAGATGACCTACATACAAATTAATTAATAAGATGCA 399
 95 -----SerProAlaValArgThrAspTyThrTyProArgTyGluThr 109
 |||||
 DB 400 AAATGTCAGACGTAACAGTGAAGTGAATGCTATGTTTAAAGATGCAAGAC 459
 110 ThrAlaGluThrThrSerGlyGlyLeuThrGlyLeuThrThrSerLeuSerThrIleu 129
 |||||
 DB 460 GTTGATCCAGCAGACGCTTGAATATGCTTATCTGTATGCTCTGTAAA-----AAT 513
 130 AlaProAlaLeuSerArgThrGlnSerAspGlySerGlySerSerSerLeu 149
 |||||
 DB 514 GGTGATGCCATTCCTAAAGGGAAGAAAGT-----AAATCAGAAATTAGA--- 558
 150 AsnIleGlyGlyMetGlyAspTyArgAsnGluThrLeuThrThrAsnProArgAspThr 169
 ::::|
 DB 559 ---ATTAAAGCAGTCACTGAT-----ACAGATTTGAATATCACTTGAAGAAAGACACA 609
 170 AlaPheLeuSerHieLeuValGln---ThrValPhePheLeuArgGlyIleAspValVal 188
 ::::|
 DB 610 CCATACCTTGTGATTAATTAGCTTTCCATCATCTTCTCCGCAACGTCAACACATGTG 669
 189 Ser-----ProAlaAsnAlaAspThrAspValPhe 198
 ::::|

DB 670 GAAAAATATGTAATAATTATGATCATCAACAGCGAAAGTGTCTAC 717

RESULT 15
 US-09-252-991A-1243
 ; Sequence 1243, Application US/09252991A
 ; Patent No. 6551795
 ; GENERAL INFORMATION:
 ; APPLICANT: Marc J. Rubenfield et al.
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 ; TITLE OF INVENTION: AERUDINOSA FOR DIAGNOSTICS AND THERAPEUTICS
 ; FILE REFERENCE: 107196.136
 ; CURRENT APPLICATION NUMBER: US/09/252,991A
 ; PRIORITY FILING DATE: 1999-02-18
 ; PRIOR APPLICATION NUMBER: US 60/074,788
 ; PRIOR FILING DATE: 1998-02-18
 ; PRIOR APPLICATION NUMBER: US 60/094,190
 ; PRIOR FILING DATE: 1998-07-27
 ; NUMBER OF SEQ ID NOS: 33142
 ; SEQ ID NO 1243
 ; LENGTH: 1491
 ; TYPE: DNA
 ; ORGANISM: Pseudomonas aeruginosa
 US-09-252-991A-1243

Alignment Scores:
 Pred. No.: 0.812 Length: 1491
 Score: 93.50 Matches: 81
 Percent Similarity: 31.65% Conservatve: 38
 Best Local Similarity: 21.54% Mismatches: 121
 Query Match: 5.68% Indels: 137
 Gaps: 18

US-10-617-835-4 (1-320) x US-09-252-991A-1243 (1-1491)

QY 12 SerValPheIleLeuSerAlaCysGlyThrLeuThrGlyIleProSerHieGlyGly 31
 |||||
 DB 154 TCGCTTTCAACCGCCAGGCGCGTGGCGCACTGAC-----GAGTACGGCGCGCA 204
 32 LysArgPheAlaValGluGlnGlyLeuValAlaIleSerAlaArgAlaValIleYsAsp 51
 ::::|
 DB 205 CCGGCC-----GTGACACAGACCTGACCCAGCGCTGAAAG----- 240
 52 MetAspLeuGlnAlaLeuHieGlyArgIleValAlaLeuTyrlleAlaThrMetGlyAsp 71
 ::::|
 DB 241 -----CACTCCTCTGAAAGAAAGGGAAGAAACGTATCTGTGATCGGCAC 291
 72 ---GlnGlySerGlySerLeuThr-----GlyGlyArg 81
 |||||
 DB 292 GGCATGGGAGACTCCGAGATGACCTGGCGGCACTACCGCGCGCGCGGCGGCTAC 351
 82 Tyr---SerIleAspAlaLeu---IleArgIleGlyTyrlleAsnSerProAlaValArg 99
 ::::|
 DB 352 TTCAAGGATTCGATGAGCTGCGGCTGACCGGCGGTACACCACTAC---TCCCTGCAC 408
 100 ThrAspTyThrTyProArgTyGluThrThrAlaGluThrThrSerGlyGlyLeuThr 119
 |||||
 DB 409 AAGGACAGCGGCTCCGCACTACGTACCGATTCGCGCGCTCCGCC-----ACC 459
 120 GlyLeuThrThrSerLeuSerThrIleuAsnAlaPro----- 131
 |||||
 DB 460 GCTGACACACCGGGGTCAAGCTGACAAAGCGCGGATGCGGTGATATCCAGCAACAG 519
 132 -----AlaLeuSerArgThrGlnSerAspGlySerGlySerArgSer 145
 ::::|
 DB 520 CCGACCGCAACCTGCTGAGCTGGCAAGCTCAACGCGCAAGGCCACGCAAGCTCTCC 579
 145 ----- 145
 580 ACCGCGAGCTGCAAGAGCCACCCCGCGCTGCTGCGCCAGTCAACGCGCTGCAAG 639
 146 -----SerLeuGlyLeuAsnIleGlyGly 153
 |||||
 DB 640 TGCTAGGTCGCGAAGCCACGACGACGACGACGACGACGACGACGACGACGACGACG 699

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Oy 154 MetGlyAspTyrArgAsnGluThrLeuThrThrAsnProArgAspThrAlaPheLeuSer 173
Db 700 GCCGGCTGATCATCCGAGCAGTGGCTGAAGACCGCCT----- 738
Oy 174 HisLeuValGlnThrValPhePheLeuArgGlyIleAspValValSerProAlaAsnAla 193
Db 739 -----GAGTGGTCTCGGGCGCGCGCC 762
Oy 194 AspThrAspValPheIleAsnIleAspValPheGlyThrIleArgAsnArgThrGluMet 213
Db 763 -----GCGACCTTCGCGAACCAGGCT 789
Oy 214 HisLeuTyrAsnAlaGluThrLeuLysAlaGlnThrLysLeu----- 227
Db 790 GCGCGCTATGCCGGGCAAGACCTTCGCGCTCAGGCCGAAAGCCCGGCTACCGGATCGTC 849
Oy 228 -----GluTyrPheAlaValAspArgThrAsnLysLysLeuIleLysPro 243
Db 850 GAGAACTCGACGAGCTGAAGCGGTGCGCGCCCAACCAAG-----CAGCCG 900
Oy 244 LysThrAsnAlaPheGluAlaIleTyrLysGluAsnTyrAlaLeuTyrMetGlyProTyr 263
Db 901 CTGATCGGCTGTTC-----GCCCGGGCAACATGCCAGTGCCTGCTCGTCCGACC 954
Oy 264 LysValSerLysGlyIleLysProThrGluGlyLeuMetValAspPheSerAspIleArg 283
Db 955 GCCACCTACCAAGC-----AACCTGAA- 977
Oy 284 ProTyrGlyAsnHisThrGlyAsnSerAlaProSerValGluAlaAspAsnSerHisGlu 303
Db 978 CCAGCCGAGC-----GGTAGCTGCGAGGCAACCGAAGCGCACCGCCGACATCCC 1028
Oy 304 GlyTyrGlyTyrSerAspGluAlaValArgGlnHisArgGlnGlyGln 319
Db 1029 GACCTGGCGCAATGACCAAGCCATCGAGCTGCTGAAGGACAA 1076
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Job time : 1983 secs

GenCore version 5.1.6
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(without alignments)
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Title: US-10-617-835-4

Perfect score: 320
Sequence: 1 MRALLPILFSLVPLSACG.....SHEGEGYDEAVRHQRCQP 320

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Ygapop 60.0 , Ygapext 60.0
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1202784 seqs, 818138359 residues

Word size: 1

Total number of hits satisfying chosen parameters: 2400006

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Maximum DB seq length: 2000000000

Post-processing: listing first 45 summaries

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-LOOPTCL=0 -LOOPTXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=oligo
-TRANS=human40.cdt -LIST=45 -DOCLIGN=200 -THR SCORE=quality -THR_MIN=1
-ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0
-MAXLEN=2000000000 -USER=US10617835.0CGN 1.1.105.0@rnuc1.18082005.115731.8766
-NCPU=6 -ICPU=3 -NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100
-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database : Issued Patents NA:

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2: /cg2_6/ptodata/1/ina/5B.COMB.seq:*
3: /cg2_6/ptodata/1/ina/6A.COMB.seq:*
4: /cg2_6/ptodata/1/ina/6B.COMB.seq:*
5: /cg2_6/ptodata/1/ina/PCITS.COMB.seq:*
6: /cg2_6/ptodata/1/ina/backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	320	100.0	1136	4	US-09-043-302-6
2	320	100.0	3287	4	US-09-043-302-1
3	8	2.5	38	4	US-09-371-772B-8146
4	8	2.5	38	4	US-09-371-772B-8900
5	8	2.5	38	4	US-09-371-772B-13757
6	8	2.5	1398	4	US-09-513-993C-16838
7	8	2.5	499	3	US-09-004-838-9
8	8	2.5	601	4	US-09-949-016-86885
9	8	2.5	601	4	US-09-949-016-105293
10	8	2.5	601	4	US-09-949-016-105294
11	8	2.5	601	4	US-09-949-016-126952
12	8	2.5	601	4	US-09-949-016-159911

C 13	8	2.5	601	4	US-09-949-016-159932	Sequence 159932.
C 14	8	2.5	636	4	US-09-902-540-8255	Sequence 8255, Ap
C 15	8	2.5	897	4	US-09-107-532A-712	Sequence 72, Appl
C 16	8	2.5	958	4	US-09-270-767-14224	Sequence 14224, A
C 17	8	2.5	966	4	US-09-252-991A-757	Sequence 757, App
C 18	8	2.5	1251	4	US-09-489-039A-3927	Sequence 3927, Ap
C 19	8	2.5	1848	1	US-08-333-802-1	Sequence 1, Appl1
C 20	8	2.5	2058	4	US-09-543-681A-310	Sequence 310, App
C 21	8	2.5	2499	4	US-09-252-991A-696	Sequence 696, App
C 22	8	2.5	2871	3	US-09-347-878-45	Sequence 45, Appl
C 23	8	2.5	2781	4	US-09-614-221A-506	Sequence 506, App
C 24	8	2.5	3026	3	US-08-981-729-6	Sequence 6, Appl1
C 25	8	2.5	3026	4	US-09-613-811-6	Sequence 719, App
C 26	8	2.5	4519	4	US-09-949-016-719	Sequence 5111, App
C 27	8	2.5	4519	4	US-09-949-016-5111	Sequence 5111, Ap
C 28	8	2.5	4637	3	US-09-921-017B-818	Sequence 818, App
C 29	8	2.5	6492	4	US-09-902-540-853	Sequence 853, App
C 30	8	2.5	7282	4	US-09-949-016-17144	Sequence 17144, A
C 31	8	2.5	16056	4	US-09-949-016-16211	Sequence 16211, A
C 32	8	2.5	16056	4	US-09-949-016-16212	Sequence 16212, A
C 33	8	2.5	26086	4	US-09-949-016-15355	Sequence 15355, A
C 34	8	2.5	26238	4	US-09-949-016-15356	Sequence 12314, A
C 35	8	2.5	40352	3	US-08-846-111D-15	Sequence 15, Appl
C 36	8	2.5	41617	4	US-09-443-077-15	Sequence 15, Appl
C 37	8	2.5	41617	4	US-09-949-016-14356	Sequence 14356, A
C 38	8	2.5	41618	4	US-09-949-016-14681	Sequence 14681, A
C 39	8	2.5	44377	2	US-08-804-222C-7	Sequence 7, Appl1
C 40	8	2.5	44377	2	US-08-804-196-1	Sequence 1, Appl1
C 41	8	2.5	93920	4	US-09-949-016-12461	Sequence 12461, A
C 42	8	2.5	93920	4	US-09-949-016-16853	Sequence 16853, A
C 43	8	2.5	247781	4	US-09-949-016-14193	Sequence 14193, A
C 44	8	2.5	247781	4	US-09-949-016-14193	Sequence 14193, A
C 45	8	2.5	536165	4	US-09-214-808-1	Sequence 1, Appl1

ALIGNMENTS

RESULT 1
US-09-043-302-6
; Sequence 6, Application US/09043302
; Patent No. 6617128
; GENERAL INFORMATION:
; APPLICANT: MEYER, Thomas F.
; APPLICANT: RUDEL, Thomas
; APPLICANT: SCHEUERPLUG, Ina
; APPLICANT: WALTER, Jurgen
; APPLICANT: EICKERNJAGER, Sandra
; TITLE OF INVENTION: Nucleic Acid Molecules Encoding Proteins Which Impart
; TITLE OF INVENTION: the Adhesion of Neisseria Cells to Human Cells
; FILE REFERENCE: 0147-172P
; CURRENT APPLICATION NUMBER: US/09/043,302
; CURRENT FILING DATE: 1998-06-08
; EARLIER APPLICATION NUMBER: PCT/EP96/04092
; EARLIER FILING DATE: 1995-09-18
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 1136
; TYPE: DNA
; ORGANISM: Neisseria gonorrhoeae
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (135)..(1094)
; US-09-043-302-6
Alignment Scores:
Pred. No.: 0
Score: 320.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
DB: 4
Length: 1136
Matches: 320
Conservative: 0
Mismatch: 0
Indels: 0
Gaps: 0

US-10-617-835-4 (1-320) X US-09-043-302-6 (1-1136)

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Qy      1 MetArgAlaArgLeuLeuIleProIleLeuPheSerValPheIleLeuSerAlaCysGly 20
Db      135 ATGGGGGACGGCTGATACCTATTTCTTTTTCGGTTTATTTATTTATTCGGCTCGGG 194
Qy      21 ThrLeuThrGlyIleProSerHisGlyGlyLysAspPheAlaValGluGluLeu 40
Db      195 ACACGTGACAGTATTCATCCATGCGGAGGAGCAACCTTCGCGGTGAAACAAGACTT 254
Qy      41 ValAlaAlaSerAlaArgAlaAlaValLysAspMetAspLeuGlnAlaLeuHisGlyArg 60
Db      255 GTGGCCGCTTCGCGACAGCTGCGCTTAAAGACATGATTTACAGGCATTTACACGACGA 314
Qy      61 LysValAlaLeuTyrIleAlaThrMetClyAspGlnGlySerGlySerLeuThrGly 80
Db      315 AAAGTTGATTTGATTCATTCGCAACTATGAGGAGCAACAGGTTGAGGACAGGGGGT 374
Qy      81 ArgTyrSerIleAspAlaLeuIleArgGlyGluTyrIleAsnSerProAlaValArgThr 100
Db      375 CGCTACTCCATTCATGACCTATTCGCGGCGAATTCATTAACAGCCCTCGCTCGGACC 434
Qy      101 AspTyrThrTyrProArgTyrGluThrThraIaGluThrThrSerGlyLysLeuThrGly 120
Db      435 GATTACACCTATCCGCTTACGAAACCAACCGCTGAAACATCATCAGCGGCTTGAACGGGT 494
Qy      121 LeuThrThrSerLeuSerThrLeuAsnAlaProAlaLeuSerArgThrGlnSerAspGly 140
Db      495 TTAAACCACTTCTTATCTTACCTTAATGCCCCCTGACCTTGCCCAACCAATCGAGCGT 554
Qy      141 SerGlySerArgSerSerLeuGlyLysAsnIleGlyGlyMetClyAspTyrArgAsnGlu 160
Db      555 AGCGAAGTAGAGACAGCTCGGCTTAATTTGGCGGAGTGGGGGANTTACGAATGAA 614
Qy      161 ThrLeuThrThrAsnProArgAspThrAlaPheLeuSerHisLeuValGlnThrValPhe 180
Db      615 ACCTTGACGACCAACCGCGCGACACTGCTTTCTTCCCTTCCCTGTTACACAGCGTATTT 674
Qy      181 PheLeuArgGlyIleAspValValSerProAlaAsnAlaAspThrAspValPheIleAsn 200
Db      675 TTCCGCGCGGACATGACGATGTTCTCTCCCAATGCGATACAGATGTTTATTTAAC 734
Qy      201 IleAspValPheGlyThrIleArgAsnArgThrGluMetHisLeuTyrAsnAlaGluThr 220
Db      735 ATCAGCGATTCGGAAGCATACGACACGAAACCGAATGACCTATTCAAATGCCGAACA 794
Qy      221 LeuLysAlaGlnThrLysLeuGluTyrPheAlaValAspArgThrAsnLysLysLeuLeu 240
Db      795 CTGAAACCCCAAAACAACTGGAAATATTTCCAGTAGACAGAACCAATAAAAAATTGCTC 854
Qy      241 IleLysProLysThrAsnAlaPheGluAlaIleAlaTyrLysGluAsnTyrAlaLeuTyrMet 260
Db      855 ATCAAAACCCAAACCAATGCTTTGAAGCTGCTTAAAGAAATTTACGACTTTGGATG 914
Qy      261 GlyProTyrLysValSerLysGlyIleLysProThrGluGlyLysMetValAspPheSer 280
Db      915 GGGCGGATTAAGTAAGTAAGTAAGTAAGTAAGTAAGTAAGTAAGTAAGTAAGTAAGTTC 974
Qy      281 AspIleArgProTyrGlyAsnHisThrGlyAsnSerAlaProSerValGluAlaAspAsn 300
Db      975 GATATTCGGGCATACGCGAATCATACGGGTAACTCCGCCCATCCGATAGAGGCGAATAC 1034
Qy      301 SerHisGluGlyTyrGlyTyrSerAspGluAlaValArgGlnHisArgGlnGlyPro 320
Db      1035 AGTCATAGGGGATGATGATACGCGATGACGAGTGCACAACTATGACAAAGGCAACT 1094
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RESULT 2
US-09-043-302-1
; Sequence 1, Application US/09043302; Patent No. 6617128
; GENERAL INFORMATION:
; APPLICANT: MEYER, Thomas F.

```
/ APPLICANT: RUDEL, Thomas
/ APPLICANT: SCHERERPLUG, Ina
/ APPLICANT: MATER, Jurgen
/ APPLICANT: EICKERMAYER, Sandra
/ APPLICANT: SCHWAN, Thomas
/ TITLE OF INVENTION: Nucleic Acid Molecules Encoding Proteins Which Impart
/ FILE REFERENCE: 0147-172P
/ CURRENT APPLICATION NUMBER: US/09/043.302
/ EARLIER APPLICATION NUMBER: PCT/EP96/04092
/ EARLIER FILING DATE: 1995-09-18
/ NUMBER OF SEQ ID NOS: 11
/ SOFTWARE: Patent In Ver. 2.0
/ SEQ ID NO: 1
/ LENGTH: 3287
/ TYPE: DNA
/ ORGANISM: Neisseria gonorrhoeae
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (136)..(447)
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (583)..(1542)
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (1585)..(3111)
/ US-09-043-302-1
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Pred. No.: 0 Length: 3287
Score: 320.00 Matches: 320
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0
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US-10-617-835-4 (1-320) X US-09-043-302-1 (1-3287)

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Qy      1 MetArgAlaArgLeuLeuIleProIleLeuPheSerValPheIleLeuSerAlaCysGly 20
Db      583 ATGGGGGACGGCTGATACCTATTTCTTTTTCGGTTTATTTATTTATTCGGCTCGGG 642
Qy      21 ThrLeuThrGlyIleProSerHisGlyGlyLysAspPheAlaValGluGluLeu 40
Db      643 ACACGTGACAGTATTCATTCATGCGGAGGAGCAACGTTCCGGGTGAAACAAGACTT 702
Qy      41 ValAlaAlaSerAlaArgAlaAlaValLysAspMetAspLeuGlnAlaLeuHisGlyArg 60
Db      703 GTGGCCGCTTCGCGACAGCTGCGCTTAAAGACATGATTTTACAGGATTTACACGACGA 762
Qy      61 LysValAlaLeuTyrIleAlaThrMetGlyAspGlnGlySerGlySerLeuThrGly 80
Db      763 AAAGTTGATTTGATTCATTCGCAACTATGAGGAGCAACAGGTTCCAGCACTTGACAGGGGT 822
Qy      81 ArgTyrSerIleAspAlaLeuIleArgGlyGluTyrIleAsnSerProAlaValArgThr 100
Db      823 CGCTACTCCATTCATGACCTATTCGCGGCGAATTCATTAACAGCCCTCGCTCGGACC 882
Qy      101 AspTyrThrTyrProArgTyrGluThrThrAlaGluThrThrSerGlyLysLeuThrGly 120
Db      883 GATTACACCTATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTC 942
Qy      121 LeuThrThrSerLeuSerThrLeuAsnAlaProAlaLeuSerArgThrGlnSerAspGly 140
Db      943 TTAAACCACTTCTTATCTTATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTC 1002
Qy      141 SerGlySerArgSerSerLeuGlyLysAsnIleGlyGlyMetClyAspTyrArgAsnGlu 160
Db      1003 AGCGAAGTAGAGACAGCTCGGCTTAAATTTGGCGGAGTGGGGGATTTATTCGAATGAA 1062
Qy      161 ThrLeuThrThrAsnProArgAspThrAlaPheLeuSerHisLeuValGlnThrValPhe 180
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Db      1063 ACCTGACGACCAACCGCGGACGACACTGCTTTCTTCCACTGTGTAAGACCGATTT 1122
Qy      181 PheleuAAGGlyIleAspValValSerProAlaAsnAlaAspThrAspValPheIleAsn 200
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Qy      201 IleAspValPheGlyThrIleArgAsnArgThrIleMetHisLeuTyrAsnAlaGluThr 220
Db      1183 ATCGACGATTTCGAAACGATTACGCAACGAAATGACCTTATACATCCGAAACCA 1242
Qy      221 LeuValaAGInThrIleLeuGluGluTyrPheAlaValAspArgThrAsnIleLeuLeu 240
Db      1243 CTGAAGCCCAAAACAACTGGAATATTTCGACATAGACAGAACCAATTAATAATTGCTC 1302
Qy      241 IleLeuProLeuThrAsnAlaPheGluAlaAlaIleTyrGluAsnTyrAlaLeuTyrMet 260
Db      1303 ATCAAAACCAAAACCAATGCGTTTGAAGCTGCTTAAAGAAATTAACGCAATTTGGATG 1362
Qy      261 GlyProTyrLeuValSerIleGlyIleLeuProThrGluGluMetValAspPheSer 280
Db      1363 GGGCGGATTAAAGTAAGCAAGCAATCAACCGACGAAAGATTAAATGTCGATTTCTCC 1422
Qy      281 AspIleArgProTyrGlyAsnHisThrGlyAsnSerAlaProSerValGluAlaAspAsn 300
Db      1423 GATATCCGCGCATACGCGCATCATACGGGTACTCGGCCCATCCGTAGAGCGTATTAAC 1482
Qy      301 SerHisGluGlyTyrGlyTyrSerAspGluAlaValAlaGlnHisArgGlnGlyGlnPro 320
Db      1483 AGTCATGAGGGGTATGATGATACGATGAAAGCAATGACGACAAATAGACCAAGGCAACCT 1542

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RESULT 3

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US-09-371-772B-8146
; Sequence 8146, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: MGSwigen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; FILE REFERENCE: MBH00, 876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8146
; LENGTH: 38
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-09-371-772B-8146

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Alignment Scores:
Pred. No.: 4.57 Length: 38
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.50% Indels: 0
DB: 4 Gaps: 0

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US-10-617-835-4 (1-320) x US-09-371-772B-8146 (1-38)
Qy      306 GlyTyrSerAspGluAlaValArg 313
Db      2 GGUUACUCUGAUGAGCGCCGUAUG 25

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RESULT 4

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US-09-371-772B-8900
; Sequence 8900, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: MGSwigen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; FILE REFERENCE: MBH00, 876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8900
; LENGTH: 38
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-09-371-772B-8900

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Alignment Scores:

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Pred. No.: 4.57 Length: 38
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.50% Indels: 0
DB: 4 Gaps: 0

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US-10-617-835-4 (1-320) x US-09-371-772B-8900 (1-38)

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Qy      306 GlyTyrSerAspGluAlaValArg 313
Db      2 GGUUACUCUGAUGAGCGCCGUAUG 25

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RESULT 5

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US-09-371-772B-13757
; Sequence 13757, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: MGSwigen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; FILE REFERENCE: MBH00, 876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 13757
; LENGTH: 38
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
NAME/KEY: misc_feature
LOCATION: (31)..(31)
OTHER INFORMATION: n stands for inosine

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US-09-371-772B-13757
Alignment Scores:
Pred. No.: 4.57      Length: 38
Score: 8.00          Matches: 8
Percent Similarity: 100.00%  Conservatives: 0
Best Local Similarity: 100.00%  Mismatches: 0
Query Match: 2.50%      Indels: 0
DB: 4                Gaps: 0

US-10-617-835-4 (1-320) x US-09-371-772B-13757 (1-38)
QY      306 G|Y|T|S|e|a|p|g|u|a|l|a|v|a|l|a|g 313
Db      2 GGCACCCUGAGGAGGCGGUAGG 25

RESULT 6
US-09-513-999C-16838
; Sequence 16838, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A. Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 16838
; LENGTH: 398
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 21
; OTHER INFORMATION: n=a, g, c or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 40
; OTHER INFORMATION: d=a or g or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 326
; OTHER INFORMATION: n=a, g, c or t
; US-09-513-999C-16838

Alignment Scores:
Pred. No.: 51.9      Length: 398
Score: 8.00          Matches: 8
Percent Similarity: 100.00%  Conservatives: 0
Best Local Similarity: 100.00%  Mismatches: 0
Query Match: 2.50%      Indels: 0
DB: 4                Gaps: 0

US-10-617-835-4 (1-320) x US-09-513-999C-16838 (1-398)
QY      116 G|Y|G|L|e|u|t|h|r|g|l|e|u|t|h|r 123
Db      140 GGAGATTGACAGGTTTGACACT 163

RESULT 7
US-09-004-838-9
; Sequence 9, Application US/09004838
; Patent No. 6350933
; GENERAL INFORMATION:
; APPLICANT: Micheltore, Richard W.
; APPLICANT: Shen, Kathy
; APPLICANT: Meyers, Blake

US-10-617-835-4 (1-320) x US-09-004-838-9 (1-499)
QY      12 S|e|V|a|P|h|e|l|e|u|S|e|r|a|C|y|S 19
Db      379 TCTGCTTATCTGTGACGATGC 402

RESULT 8
US-09-949-016-86885/C
; Sequence 86885, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08

TITLE OF INVENTION: Procedures and Materials for
NUMBER OF INVENTION: Confering Pest Resistance in Plants
NUMBER OF SEQUENCES: 140
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/004,838
FILING DATE: 09-JAN-1998
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/781,734
FILING DATE: 10-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Einhorn, Gregory P.
REGISTRATION NUMBER: 38,440
REFERENCE/DOCKET NUMBER: 023070-078810US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 499 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: -
LOCATION: 1..499
OTHER INFORMATION: /note="R|G|I"

US-09-004-838-9

Alignment Scores:
Pred. No.: 65.5      Length: 499
Score: 8.00          Matches: 8
Percent Similarity: 100.00%  Conservatives: 0
Best Local Similarity: 100.00%  Mismatches: 0
Query Match: 2.50%      Indels: 0
DB: 3                Gaps: 0
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; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for windows Version 4.0
; SEQ ID NO 86885
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-86885

Alignment Scores:
Pred. No.: 79.4      Length: 601
Score: 8.00          Matches: 8
Percent Similarity: 100.00%  Conservative: 0
Best Local Similarity: 100.00%  Mismatches: 0
Query Match: 2.50%      Indels: 0
DB: 4                Gaps: 0

US-10-617-835-4 (1-320) x US-09-949-016-86885 (1-601)

Qy 74 SerGlySerLeuThrGlyGlyArg 81
Db 570 TCCGGCTCAGTCCAGTGGAGG 547

RESULT 9
US-09-949-016-105293/c
; Sequence 105293, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for windows Version 4.0
; SEQ ID NO 105293
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-105293

Alignment Scores:
Pred. No.: 79.4      Length: 601
Score: 8.00          Matches: 8
Percent Similarity: 100.00%  Conservative: 0
Best Local Similarity: 100.00%  Mismatches: 0
Query Match: 2.50%      Indels: 0
DB: 4                Gaps: 0

US-10-617-835-4 (1-320) x US-09-949-016-105293 (1-601)

Qy 15 IleuSerAlaCyaeGlyThrIeu 22
Db 418 ATTCACAGTGCCTGTGGTACATTA 395

RESULT 10
US-09-949-016-105294/c
; Sequence 105294, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
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; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for windows Version 4.0
; SEQ ID NO 105294
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-105294

Alignment Scores:
Pred. No.: 79.4      Length: 601
Score: 8.00          Matches: 8
Percent Similarity: 100.00%  Conservative: 0
Best Local Similarity: 100.00%  Mismatches: 0
Query Match: 2.50%      Indels: 0
DB: 4                Gaps: 0

US-10-617-835-4 (1-320) x US-09-949-016-105294 (1-601)

Qy 15 IleuSerAlaCyaeGlyThrIeu 22
Db 68 ATTCACAGTGCCTGTGGTACATTA 45

RESULT 11
US-09-949-016-126952
; Sequence 126952, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for windows Version 4.0
; SEQ ID NO 126952
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-126952

Alignment Scores:
Pred. No.: 79.4      Length: 601
Score: 8.00          Matches: 8
Percent Similarity: 100.00%  Conservative: 0
Best Local Similarity: 100.00%  Mismatches: 0
Query Match: 2.50%      Indels: 0
DB: 4                Gaps: 0

US-10-617-835-4 (1-320) x US-09-949-016-126952 (1-601)

Qy 141 SerGlySerArgSerSerIeuGly 148
Db 373 AGTGGTGCAGATCCAGCTGGGT 396

RESULT 12
US-09-949-016-159911/c
; Sequence 159911, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
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; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 159911
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-159911

Alignment Scores:
Pred. No.: 79.4      Length: 601
Score: 8.00      Matches: 8
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match: 2.50%      Indels: 0
DB: 4      Gaps: 0

US-10-617-835-4 (1-320) x US-09-949-016-159911 (1-601)

Qy 140 GlySerGlySerArgSerSerLeu 147
Db 197 GGGAGCGGAGACAGTCTCCCTC 174

RESULT 13
US-09-949-016-159932/c
; Sequence 159932, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 159932
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-159932

Alignment Scores:
Pred. No.: 79.4      Length: 601
Score: 8.00      Matches: 8
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match: 2.50%      Indels: 0
DB: 4      Gaps: 0

US-10-617-835-4 (1-320) x US-09-949-016-159932 (1-601)

Qy 140 GlySerGlySerArgSerSerLeu 147
Db 197 GGGAGCGGAGACAGTCTCCCTC 174

RESULT 14
US-09-902-540-8255
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; Sequence 8255, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(115849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 8255
; LENGTH: 636
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-8255

Alignment Scores:
Pred. No.: 84.2      Length: 636
Score: 8.00      Matches: 8
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match: 2.50%      Indels: 0
DB: 4      Gaps: 0

US-10-617-835-4 (1-320) x US-09-902-540-8255 (1-636)

Qy 41 ValAlaAlaSerAlaArgAlaAla 48
Db 270 GTGCGGGCTTCGCTCGAGCTGCC 293

RESULT 15
US-09-107-532A-72
; Sequence 72, Application US/09107532A
; Patent No. 6583275
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 7310
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM ISO9660
; COMPUTER: PC
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,532A
; FILING DATE: 30-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/085,598
; FILING DATE: 14 May 1998
; APPLICATION NUMBER: 60/051571
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ariniello, Pamela Deneke
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-5007
; TELEFAX: (781)893-8277
; INFORMATION FOR SEQ ID NO: 72:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 897 base pairs
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:      TYPE: nucleic acid
:      STRANDEDNESS: double
:      TOPOLOGY: circular
:      MOLECULE TYPE: DNA (genomic)
:      HYPOTHETICAL: NO
:      ANTI-SENSE: NO
:      ORIGINAL SOURCE:
:      ORGANISM: Enterococcus faecium
:      FEATURE:
:      NAME/KEY: misc_feature
:      LOCATION: (B) LOCATION 1...897
:      SEQUENCE DESCRIPTION: SEQ ID NO: 72:
US-09-107-532A-72

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Alignment Scores:
Pred. No.:      120      Length:      897
Score:          8.00      Matches:      8
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match:      2.50%      Indels:      0
DB:                4      Gaps:          0

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US-10-617-835-4 (1-320) x US-09-107-532A-72 (1-897)

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Db      103 TTATTTTAAGCGCTTGCGTACA 126

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Search completed: August 19, 2005, 01:21:23
 Job time : 160 secs

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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus.p2n model

Run on: August 19, 2005, 01:39:13 ; Search time 650 Seconds

(without alignments)
3196.463 Million cell updates/sec

Title: US-10-617-835-4

Perfect score: 320

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Ygapop 60.0 , Ygapext 60.0

Fgapop 6.0 , Fgapext 7.0

Delop 6.0 , Delext 7.0

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Word size: 1

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-DB=Published Applications NA -QMT=faescap -SUFFIX=p2noligo.rmpb -MINMATCH=0.1

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-TRANS=human40.cdi -LIST=45 -DOCLIGN=200 -THR SCORE=quality -THR MIN=1

-ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0

-MAXLEN=200000000 -USER=US1061735_@CGN_1_1_723_@runat_18082005_115732_8783

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-FGAPOP=6 -FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

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Published Applications NA:

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21: /cgn2_6/ptodata/2/pubpna/US10I_PUBCOMB.seq:

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23: /cgn2_6/ptodata/2/pubpna/US10K_PUBCOMB.seq:

24: /cgn2_6/ptodata/2/pubpna/US10L_PUBCOMB.seq:

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and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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4	320	100.0	1136	22	US-10-617-835-1
5	21	6.6	939	17	US-10-320-800-69
6	10	3.1	2505	13	US-10-027-632-252306
7	10	3.1	2505	17	US-10-027-632-252306
8	10	3.1	24173	14	US-09-764-891-5294
9	10	3.1	24173	14	US-10-091-572-855
10	9	2.8	463	20	US-10-437-963-48432
11	9	2.8	463	20	US-10-425-115-122322
12	9	2.8	530	20	US-10-425-115-137587
13	9	2.8	2849	9	US-09-823-245A-481
14	9	2.8	12705	15	US-10-311-455-122
15	9	2.8	16720	15	US-10-311-455-388
16	9	2.8	16720	17	US-10-221-613-76
17	9	2.8	822900	17	US-10-292-798-1393
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20	8	2.5	38	10	US-09-846-754A-4546
21	8	2.5	38	10	US-09-846-754A-5718
22	8	2.5	38	10	US-09-780-164-1432
23	8	2.5	38	10	US-09-792-818-966
24	8	2.5	38	18	US-10-138-674-10423
25	8	2.5	38	18	US-10-138-674-11177
26	8	2.5	38	18	US-10-138-674-16034
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29	8	2.5	38	19	US-10-287-949A-16034
30	8	2.5	136	16	US-10-029-386-17322
31	8	2.5	187	20	US-10-425-115-47882
32	8	2.5	201	21	US-10-741-600-3544
33	8	2.5	201	21	US-10-741-600-3574
34	8	2.5	201	21	US-10-741-600-3574
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37	8	2.5	261	18	US-10-424-599-1531
38	8	2.5	294	10	US-09-814-353-4759
39	8	2.5	306	10	US-09-814-353-11056
40	8	2.5	324	18	US-10-425-115-35343
41	8	2.5	329	20	US-10-425-115-184382
42	8	2.5	351	10	US-09-814-353-17440
43	8	2.5	366	19	US-10-437-963-68284
44	8	2.5	395	10	US-09-918-995-34354
45	8	2.5	400	9	US-09-960-352-8074

ALIGNMENTS

RESULT 1
US-09-043-302-6
; Sequence 6, Application US/09043302
; Publication No. US20020086349A1
GENERAL INFORMATION:
APPLICANT: MEYER, Thomas F.
APPLICANT: RUDEU, Thomas
APPLICANT: SCHERREPLUG, Ina
APPLICANT: WAIER, Jurgen
APPLICANT: EICKENJAGER, Sandra
APPLICANT: SCHWAB, Thomas
TITLE OF INVENTION: Nucleic Acid Molecules Encoding Proteins Which Impart
FILE REFERENCE: 0147-172P
CURRENT APPLICATION NUMBER: US/09/043.302
CURRENT FILING DATE: 1998-06-08

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; EARLIER APPLICATION NUMBER: PCT/EP96/04092
; EARLIER FILING DATE: 1995-09-18
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 1136
; TYPE: DNA
; ORGANISM: Neisseria gonorrhoeae
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (135)..(1094)
US-09-043-302-6

Alignment Scores:
Pred. No.: 0 Length: 1136
Score: 320.00 Matches: 320
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-10-617-835-4 (1-320) x US-09-043-302-6 (1-1136)
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QY 21 ThrLeuThrGlyIleProSerHisGlyGlyGlyValAspPheAlaValGluGluLeu 40
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QY 41 ValAlaAlaSerAlaArgAlaAlaValIysAspMetAspLeuGlnAlaLeuHisGlyArg 60
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QY 61 LysValAlaLeuTyrIleAlaThrMetGlyAspGlnGlySerGlySerLeuThrGlyGly 80
Db 315 AAAGTTGATTTGATTCATTCGCACTATGGCGCAGCAAGGTTTCAGGCACTTTCAGAGGGGT 374
QY 81 ArgTyrSerIleAspAlaLeuIleArgGlyGluTyrIleAsnSerProAlaValArgThr 100
Db 375 CGCTACTCATTTGATGACTGATGTTGCGGCGAATACATAACAGCCCTGCGCTCGCACCC 434
QY 101 AspTyrThrTyrProArgTyrGluThrThrAlaGluThrThrSerGlyLeuThrGly 120
Db 435 GATTACACCTATCCGCGTTACGAAACCAACCGCTGAACACATCAGCGGTTTTCAGCGGT 494
QY 121 LeuThrThrSerLeuSerThrLeuAsnAlaProAlaLeuSerAlaGlnSerAspGly 140
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QY 141 SerGlySerArgSerSerLeuGlyLeuAsnIleGlyGlyMetGlyAspTyrArgAsnGlu 160
Db 555 AGCGGAAGTACGACAGCTGCGGCTTAATTTGGCGGGAATGGGGGATTATCGAAATGAA 614
QY 161 ThrLeuThrThrAsnProArgAspThrAlaPheLeuSerHisGlyValGlnThrValPhe 180
Db 615 ACCTTGACGACCAACCGCGGACGACCTGCTTTTCCACTGCTGTTACACACCGTATTT 674
QY 181 PheLeuArgGlyIleAspValValSerProAlaAsnAlaAspThrAspValPheIleAsn 200
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QY 201 IleAspValPheGlyThrIleArgAsnArgThrGluMetHisGlyTyrAsnAlaGluThr 220
Db 735 ATCAACGATTCGAGACGATACGCAACGAAACCGAAATGCACTTATACATGCGGAAACA 794
QY 221 LeuIysAlaGlnThrIysLeuGluIuTyrPheAlaValAspArgThrAsnIysLeuLeu 240
Db 795 CTGAAAGCCCAAACTGGAATATTTCCAGATGACAGAACCAATTAATAAATTTGCTC 854
QY 241 IleLysProLysThrAsnAlaPheGluAlaAlaTyrIysGluAsnTyrAlaLeuTyrMet 260

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Db 855 ATCAAAACCAAAACCAATGCGTTTGAAGCTGCTTAAAGAAATTAACGATTTGTGATG 914
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Db 915 GGGCCGATTAAGTAAAGTAAAGCAAGGATCAACCGAGGAAAGATTAAATGTCGATTTCTCC 974
QY 281 AspIleArgProTyrGlyAsnHisThrGlyAsnSerAlaProSerValGluAlaAspAsn 300
Db 975 GATATCCGGCCATACGCGCAATCATACGGGTAACTCCGCCCATTCGTAGAGGCTGATTAAC 1034
QY 301 SerHisGlyGlyTyrGlyTyrSerAspGluAlaValArgGlnHisArgGlnGlyPro 320
Db 1035 AGTCATGAGGGGTATGATACAGCATGAAAGAGTGGCAACATAGACAAGGGCAACT 1094

RESULT 2
US-10-617-835-6
; Sequence 6, Application US/10617835
; Publication No. US20050124037A1
; GENERAL INFORMATION:
; APPLICANT: MEYER, Thomas F.
; APPLICANT: RUDEL, Thomas
; APPLICANT: SCHEUERPLUG, Ina
; APPLICANT: MATER, Jürgen
; APPLICANT: EICKENUDGER, Sandra
; APPLICANT: SCHWAN, Thomas
; TITLE OF INVENTION: Nucleic Acid Molecules Encoding Proteins Which Impart
; TITLE OF INVENTION: the Adhesion of Neisseria Cells to Human Cells
; FILE REFERENCE: 0147-172P
; CURRENT FILING DATE: 2003-07-14
; PRIOR FILING DATE: 2003-07-14
; PRIOR APPLICATION NUMBER: US/09/043,302
; PRIOR FILING DATE: 1998-06-08
; PRIOR APPLICATION NUMBER: PCT/EP96/04092
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 1136
; TYPE: DNA
; ORGANISM: Neisseria gonorrhoeae
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (135)..(1094)
US-10-617-835-6

Alignment Scores:
Pred. No.: 0 Length: 1136
Score: 320.00 Matches: 320
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 22 Gaps: 0

US-10-617-835-4 (1-320) x US-10-617-835-6 (1-1136)
QY 1 MetArgAlaArgLeuLeuIleProIleLeuPheSerValPheIleLeuSerAlaCysGly 20
Db 135 ATGCGGGACCGGCTGCTGATACCTATCTTTTTCGGTTTATTTATTCGCCCTGCCGG 194
QY 21 ThrLeuThrGlyIleProSerHisGlyGlyGlyValAspPheAlaValGluGluLeu 40
Db 195 ACACGACAGGATTTCCATCGCATGCGGAGCGAAACGTTTCGCGGTGAACAGAACTT 254
QY 41 ValAlaAlaSerAlaArgAlaAlaValIysAspMetAspLeuGlnAlaLeuHisGlyArg 60
Db 255 GTGGCCGCTTCTGCGCAGAGCTGCCGTTAAAGCATGATTTAAAGCATTTACAGGCACTTAC 314
QY 61 LysValAlaLeuTyrIleAlaThrMetGlyAspGlnGlySerGlySerLeuThrGlyGly 80
Db 315 AAAGTTGATTTGATTCATTCGCACTATGGCGCAGCAAGGTTTCAGGCACTTTCAGAGGGGT 374
QY 81 ArgTyrSerIleAspAlaLeuIleArgGlyGluTyrIleAsnSerProAlaValArgThr 100

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Db 375 CGTACTCCATTGATGACTGATGCGGGCAATACATAACAGCCCTGCGGCACC 434
Qy 101 AAPTYYRTHRYPRXARGYRGILUTHRTHRAAGLUTHRTHSergIyGlyLeuThrGly 120
Db 435 GATTACACTTACCGCGTTACGAAACACCGCTGAAACAAATCAGCGCGTTGACGGGT 494
Qy 121 LeuThrTrhSerLeuSerThrLeuAaAaPProAlaLeuSerArgThrGlnSerAapGly 140
Db 495 TTAAACCACTTCTTTATCTACACTTAATGCGCTGCACTTCCGCAACCAATCAACGGT 554
Qy 141 SerGlySerArgSerSerLeuGlyLeuAaAaIleGlyGlyMetGlyAapTrArgAaGlu 160
Db 555 AGCGGAAGTAGAGAGCTGCGCTTAATAATTGCGGGATGGGGGATTAATGGAATGA 614
Qy 161 ThrLeuThrTrhAaAaProArgAaPThrAlaPheLeuSerHisLeuValGlnThrValPhe 180
Db 615 ACCTTGAGACACCAACCGCGCGACACTGCTTCTTCCACTTGCTGACAGCCGTAATT 674
Qy 181 PheLeuAArgGlyIleAaPValAaIleSerProAlaAaAaAaAaPThrAaPValPheIleAa 200
Db 675 TTCCTGCGCGCATAGACGTTTCTCTGCGCAATGCGCATACAGATGTTTATTAC 734
Qy 201 IleAaPValPheGlyThrIleArgAaAaArgThrgIuMetHisLeuTrArgAaAaGluThr 220
Db 735 ATCGACGATTCGGAACGATACGCAACAGAACCGAAATGCACCTATTAACATGCCAACA 794
Qy 221 LeuysAaIaGlnThrIleLeuGluGlyLutyrPheAlaValAaAaPThrAaAaIleLeuLeu 240
Db 795 CTGAAAGCCCAAAACCAACTGGAATATTTGCGATGACAGAACCAATTAATAATTTGCTC 854
Qy 241 IleLeuPProLySerThraAaAaIlePheGluAaAaIleAaIleAaAaAaAaAaAaAa 260
Db 855 ATCAAAACCAAAACCAATGCGCTTGAAGCTGCTTAAGAAATTAAGCAATGCGATG 914
Qy 261 GlyProTyrLySValSerIleGlyIleuysProThrgIuGlyLeuMetValAaPheSer 280
Db 915 GGGCGCGTAAAGTAAGTAAGAAATCAAAACCGAAGGATTAATGTCATTTCTCC 974
Qy 281 AaPThrAaPProTyrGlyAaAaAaIlePheGlyAaAaAaAaAaAaAaAaAaAaAaAa 300
Db 975 GATATCCGCGCATAGCGCAATCATATGCGGTAACTCGCCCATCGTGAAGCGTATTAAC 1034
Qy 301 SerHisGlyGlyIleGlyIleuysAaPProGluAaAaIleAaAaAaAaAaAaAaAa 320
Db 1035 AGTCATGAGGGGTATGATACAGCAATGACGATGCAACATAGCAAGGCAACCT 1094

RESULT 3
US-09-043-302-1
; Sequence 1, Application US/09043302
; Publication No. US20020086349A1
; GENERAL INFORMATION:
; APPLICANT: MEYER, Thomas F.
; APPLICANT: RUDEL, Thomas
; APPLICANT: SCHUEBERPFLUG, Ina
; APPLICANT: MAIER, Jurgen
; APPLICANT: EICKERNJAGER, Sandra
; APPLICANT: SCHWAN, Thomas
; TITLE OF INVENTION: Nucleic Acid Molecules Encoding Proteins Which Impart
; TITLE OF INVENTION: the Adhesion of Neisseria Cells to Human Cells
; FILE REFERENCE: 0147-172P
; CURRENT APPLICATION NUMBER: US/09/043,302
; EARLIER FILING DATE: 1998-06-08
; EARLIER APPLICATION NUMBER: PCT/EP96/04092
; EARLIER FILING DATE: 1995-09-18
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 3287
; TYPE: DNA
; ORGANISM: Neisseria gonorrhoeae
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (136)..(447)

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; FEATURE:
; NAME/KEY: CDS
; LOCATION: (583)..(1542)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1585)..(3111)
US-09-043-302-1

Alignment Scores:
Pred. No.: 0
Score: 320.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
DB: 9 Gaps: 0

US-10-617-835-4 (1-320) x US-09-043-302-1 (1-3287)

Qy 1 MetArgAlaArgLeuLeuIleProIleuPheSerValPheIleuSerAlaCysGly 20
Db 583 ATGCGGAGCGAGCTGCTGATACCTATTTCTTTTTCGTTTATTTATTCGCGCTGCGG 642
Qy 21 ThrLeuThrGlyIleProSerHisGlyGlyLySArgPheAlaValGluGlnGluLeu 40
Db 643 AACACTGACAGGATTCATCGCATGCGGAGGCAAAAGCTTCGCGGTGAAACAACTT 702
Qy 41 ValAlaAaAaSerAlaArgAlaAlaValAaAaPheAaPheLeuGlnAlaLeuHisGlyArg 60
Db 703 GTGGCGGCTTGTGCGACAGCTGCGGTAAACAATGATTAACAGCAATTAACAGCAATTA 762
Qy 61 LysValAlaLeuTyrIleAlaIleThrMetGlyAaPProGlnGlySerLeuThrGlyGly 80
Db 763 AAAGTGTGATTCATTCATTCGCACTATGCGGCAACCAAGCTTCAGGCAATTTGACAGGG 822
Qy 81 ArgTyrSerIleAaPProAaAaIleuIleArgGlyGluTyrIleAaAaAaAaAaAaAaAa 100
Db 823 CGTACTCCATTGATGACTGATTCGCGGCAATACATTAACAGCCCTGCGTCCGAC 882
Qy 101 AAPTYYRTHRYPRXARGYRGILUTHRTHRAAGLUTHRTHSergIyGlyLeuThrGly 120
Db 883 GATTACACTTATCCGCGTTAGAAACCAACCGCTGAAACAAATCAAGGCGGTTTGACGGGT 942
Qy 121 LeuThrTrhSerLeuSerThrLeuAaAaAaPProAlaLeuSerArgThrGlnSerAapGly 140
Db 943 TTAAACCACTTCTTTATCTACACTTAATGCCCTGCACTTCCGCAACCAATCAACGGT 1002
Qy 141 SerGlySerArgSerSerLeuGlyLeuAaAaIleGlyGlyMetGlyAapTrArgAaGlu 160
Db 1003 AGCGGAAGTAGAGAGCTGCGCTTAATAATTGCGGGATGGGGGATTAATGGAATGA 1062
Qy 161 ThrLeuThrTrhAaAaProArgAaPThrAlaPheLeuSerHisLeuValGlnThrValPhe 180
Db 1063 ACCTTGAGACCAACCGCGCGACACTGCTTCTTCCACTTGCTGACAGCCGTAATT 1122
Qy 181 PheLeuAArgGlyIleAaPValAaIleSerProAlaAaAaAaAaPThrAaPValPheIleAa 200
Db 1123 TTCCTGCGCGCATAGACGTTTCTCTGCGCAATGCGCATACAGATGTTTATTAC 1182
Qy 201 IleAaPValPheGlyThrIleArgAaAaArgThrgIuMetHisLeuTrArgAaAaGluThr 220
Db 1183 ATCGACGATTCGGAACGATACGCAACAGAACCGAAATGCACTATTAACAAAGCCGAAACA 1242
Qy 221 LeuysAaIaGlnThrIleLeuGluGlyLutyrPheAlaValAaAaPThrAaAaIleLeuLeu 240
Db 1243 CTGAAAGCCCAAAACCAACTGGAATATTTCCAGATGACAGAACCAATTAATAATTTGCTC 1302
Qy 241 IleLeuPProLySerThraAaAaIlePheGluAaAaIleAaIleAaAaAaAaAaAaAa 260
Db 1303 ATCAAAACCAAAACCAATGCGCTTGAAGCTGCTTAAGAAATTAAGCAATGCGATG 1362
Qy 261 GlyProTyrLySValSerIleGlyIleuysProThrgIuGlyLeuMetValAaPheSer 280
Db 1363 GGGCGGTATTAAGTAAGTAAGAAATCAAAACCGAAGGATTAATGTCGATTTCTCC 1422

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Qy 281 AsplleargProtyrGlyAsnHietHrGlyAsnSerAlaProSerValGluAlaAspAsn 300
Db 1423 GATATCCGGCCATACGGCAATCATACGGGTAACTCCGCCATCCGTAGAGGCTGATTAAC 1482
Qy 301 SerHiegluglyTyrrGlyTyrrSerAspGluAlaValArglnHietArglnGlyGlnPro 320
Db 1483 AGTCATGAGGGGTATGATGATACAGCGATGAACAGTGCACAACTAGACAAAGGCGAACTT 1542

RESULT 4
US-10-617-835-1
; Sequence 1, Application US/10617835
; Publication No. US20050124037A1
; GENERAL INFORMATION:
; APPLICANT: MEYER, Thomas F.
; APPLICANT: RUDEL, Thomas
; APPLICANT: SCHEUERPFUG, Ina
; APPLICANT: MATER, Jürgen
; APPLICANT: EICKERNJAGER, Sandra
; APPLICANT: SCHWAN, Thomas
; TITLE OF INVENTION: Nucleic Acid Molecules Encoding Proteins Which Impart
; TITLE OF INVENTION: the Adhesion of Neisseria Cells to Human Cells
; FILE REFERENCE: 0147-172P
; CURRENT APPLICATION NUMBER: US/10/617, 835
; CURRENT FILING DATE: 2003-07-14
; PRIOR APPLICATION NUMBER: US/09/043,302
; PRIOR FILING DATE: 1998-06-08
; PRIOR APPLICATION NUMBER: PCT/EP96/04092
; PRIOR FILING DATE: 1995-09-18
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 3287
; TYPE: DNA
; ORGANISM: Neisseria gonorrhoeae
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (136)..(447)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (583)..(1542)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1585)..(3111)
US-10-617-835-1

Alignment Scores:
Pred. No.: 0 Length: 3287
Score: 320.00 Matches: 320
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 22 Gaps: 0

US-10-617-835-4 (1-320) x US-10-617-835-1 (1-3287)
Qy 1 MeArGlaaArgLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 20
Db 583 ATGGCGGACGCGCTGCTGATACCTATCTTTTTCGCTTTTATTTATTCGCGCTGCGG 642
Qy 21 ThrLeuThrglyIleProSerHieglYgIyGlyTyrrAspPheAlaValGlnGlnLeu 40
Db 643 ACACTGACAGGTATTCATCGCATGCGGAGCAAAAGCTTCGCGTGCAGACAAAGAACTT 702
Qy 41 ValAlaAlaSerAlaArgAlaValAlaValAspMetAspLeuGlnAlaLeuHieglYArg 60
Db 703 GTGGCCCTTCTGCGACAGCTGCCGTAAAGACATGATTTTACAGGCATTACAGGAGCA 762
Qy 61 LysValAlaLeuTyrrIleAlaThMeGlyAspGlnGlySerGlySerLeuThrglyGly 80
Db 763 AAAGTTGATTGATTCATTGCACTATGCGGCAACCAAGTTTACGACAGTTTACAGGGGCT 822
Qy 81 ArgTyrrSerIleAspAlaLeuIleArgGlyGlyIleuTyrrIleAsnSerProAlaValArgThr 100
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Db 823 CGCTACTCCATTGATGATGATTCGCGGCAATACATAAAGCCCTGCGCTCCGACCC 882
Qy 101 AspTyrrThrTyrrProArgTyrrGlyThrThrAlaGlnThrThrSerGlyGlyLeuThrgly 120
Db 883 GATTACACCTATCCGCTTACGAAACCAACCGCTGAAACCAATCAGGCGGTTTACCGGCT 942
Qy 121 LeuThrThrSerLeuSerThrLeuAsnAlaProAlaLeuSerArgThrglnSerAspGly 140
Db 943 TTAAACACTCTTTATATATACACTTAATGCCCTGCACCTTCGCGCACCAATCAGACGCT 1002
Qy 141 SerGlySerArgSerSerLeuGlyLeuAsnHieglYgIyMetGlyAspTyrrArgAsnGlu 160
Db 1003 AGCGGAAGTGAAGCACTCTGGGCTTAAATTCGCGGATGGGGATTTTCGAAATGAA 1062
Qy 161 ThrLeuThrThrAspProArgAspThrAlaPheLeuSerHieglYgIyGlnThrValPhe 180
Db 1063 ACCTTGACGACCAACCCGCGGACACTGCTTTTCCCATTTGTCAGACCGGTATTT 1122
Qy 181 PheLeuArgGlyIleAspValIleSerProAlaAsnAlaAspThrAspValPheIleAsn 200
Db 1123 TTCCGCGCGGCATAGACGTTGTTTCTCGCCAAATCCGATACAGATGTGTTATTATTAAC 1182
Qy 201 IleAspValPheGlyThrIleArgAsnArgThrglyMetHieglYgIyGlnThrValPhe 220
Db 1183 ATCGACCTATTCGGAACGATACGCAACAGAACCAATGACCTTATCAATGCCGAACA 1242
Qy 221 LeuValAlaGlnThrIleValGluTyrrPheAlaValAspArgThrAsnIleValLeuLeu 240
Db 1243 CTGAAGCCCAACAAACCTGGAATATTTTCGACTAGACGAACCAATTAATAATTTCTC 1302
Qy 241 IleValProLysThrAsnAlaPheGluAlaAlaTyrrGlnLeuGlnTyrrAlaLeuTyrrMet 260
Db 1303 ATCAAAACCAAAACCAATGCGTTTGAAGCTGCTTAATAAGAAATTCGCAATGTGGATG 1362
Qy 261 GlyProTyrrIleValSerIleGlyIleValProThrglyGlnGlyLeuMetValAspPheSer 280
Db 1363 GGGCGGTATTAAGTAAGCAAGGATCAACCGACGGAAGATTAATGATGATTTCTCC 1422
Qy 281 AsplleargProtyrGlyAsnHietHrGlyAsnSerAlaProSerValGluAlaAspAsn 300
Db 1423 GATATCCGGCCATACGGCAATCATACGGGTAACTCCGCCATCCGTAGAGGCTGATTAAC 1482
Qy 301 SerHiegluglyTyrrGlyTyrrSerAspGluAlaValArglnHietArglnGlyGlnPro 320
Db 1483 AGTCATGAGGGGTATGATGATACAGCGATGAACAGTGCACAACTAGACAAAGGCGAACTT 1542

RESULT 5
US-10-320-800-69
; Sequence 69, Application US/10320800
; Publication No. US20030215469A1
; GENERAL INFORMATION:
; APPLICANT: ROBINSON, ANDREW
; APPLICANT: GORRINGE, ANDREW
; APPLICANT: HUDSON, MICHAEL
; APPLICANT: REDDIN, KAREN
; TITLE OF INVENTION: MULTICOMPONENT MENINGOCOCCAL VACCINE
; FILE REFERENCE: 1581.0790001
; CURRENT APPLICATION NUMBER: US/10/320, 800
; CURRENT FILING DATE: 2002-12-17
; PRIOR APPLICATION NUMBER: PCT/GB99/03626
; PRIOR FILING DATE: 1999-11-02
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 69
; LENGTH: 939
; TYPE: DNA
; ORGANISM: Neisseria meningitidis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(939)
; OTHER INFORMATION: NMB0652 maf A
US-10-320-800-69
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Alignment Scores:
Pred. No.: 2,01e-11 Length: 939
Score: 21.00 Matches: 21
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 6.56% Indels: 0
DB: 17 Gaps: 0

US-10-617-835-4 (1-320) x US-10-320-800-69 (1-939)

Oy 214 HisLeuTYrAsnAlaGluThrLeuLysAlaGlnThrLysLeuGluTYrPheAlaValAsp 233
Db 628 CACCTCTGAAAGCGCGAAACCTTAAAGCCCAACCAAGCTGATATTTCGCCCTGAC 687

Oy 234 Arg 234
Db 688 CGC 690

RESULT 6
US-10-027-632-252306/c
; Sequence 252306, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT FILING DATE: 2002-04-30
; PRIOR FILING DATE: 2002-04-30
; PRIOR FILING DATE: 2000-07-12
; PRIOR FILING DATE: 2000-07-12
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 252306
; LENGTH: 2505
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-252306

Alignment Scores:
Pred. No.: 12.1 Length: 2505
Score: 10.00 Matches: 10
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.12% Indels: 0
DB: 13 Gaps: 0

US-10-617-835-4 (1-320) x US-10-027-632-252306 (1-2505)

Oy 4 ArgLeuLeuIleProIleLeuPheSerVal 13
Db 571 AGACTCTTGATACCGATTTTATTTCGGTG 542

RESULT 7
US-10-027-632-252306/c
; Sequence 252306, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT FILING DATE: 2002-04-30
; PRIOR FILING DATE: 2002-04-30
; PRIOR FILING DATE: 2000-07-12
; PRIOR FILING DATE: 2000-07-12
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 252306
; LENGTH: 2505
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-252306

Alignment Scores:
Pred. No.: 12.1 Length: 2505
Score: 10.00 Matches: 10
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.12% Indels: 0
DB: 17 Gaps: 0

US-10-617-835-4 (1-320) x US-10-027-632-252306 (1-2505)

Oy 4 ArgLeuLeuIleProIleLeuPheSerVal 13
Db 571 AGACTCTTGATACCGATTTTATTTCGGTG 542

RESULT 8
US-09-764-891-9294
; Sequence 9294, Application US/09764891
; Publication No. US20030077808A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC006
; CURRENT FILING DATE: 2001-01-17
; PRIOR APPLICATION data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 10231
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9294
; LENGTH: 24173
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-891-9294

Alignment Scores:
Pred. No.: 94.4 Length: 24173
Score: 10.00 Matches: 10
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.12% Indels: 0
DB: 10 Gaps: 0

US-10-617-835-4 (1-320) x US-09-764-891-9294 (1-24173)

Oy 140 GlySerGlySerArgSerSerLeuGlyLeu 149
Db 19606 GGCTCAGGCTTCAGTCTCTCTCGGCGCTT 19635

RESULT 9
US-10-091-572-855
Sequence 855, Application US/10091572
Publication No. US20030054373A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PA118C1
CURRENT FILING DATE: US/10/091,572
CURRENT FILING DATE: 2002-03-07
PRIOR APPLICATION NUMBER: 09/764,850
PRIOR FILING DATE: 2001-01-17
PRIOR APPLICATION NUMBER: 60/179,065
PRIOR FILING DATE: 2000-01-31
PRIOR APPLICATION NUMBER: 60/180,628
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: 60/214,886
PRIOR FILING DATE: 2000-06-28
PRIOR APPLICATION NUMBER: 60/217,487
PRIOR FILING DATE: 2000-07-11
PRIOR APPLICATION NUMBER: 60/225,758
PRIOR FILING DATE: 2000-08-14
PRIOR APPLICATION NUMBER: 60/220,963
PRIOR FILING DATE: 2000-07-26
PRIOR APPLICATION NUMBER: 60/217,496
PRIOR FILING DATE: 2000-07-11
PRIOR APPLICATION NUMBER: 60/225,447
PRIOR FILING DATE: 2000-08-14
PRIOR APPLICATION NUMBER: 60/218,290
PRIOR FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: 60/225,757
PRIOR FILING DATE: 2000-08-14
PRIOR APPLICATION NUMBER: 60/226,868
PRIOR FILING DATE: 2000-08-22
PRIOR APPLICATION NUMBER: 60/216,647
PRIOR FILING DATE: 2000-07-07
PRIOR APPLICATION NUMBER: 60/225,267
PRIOR FILING DATE: 2000-08-14
PRIOR APPLICATION NUMBER: 60/216,880
PRIOR FILING DATE: 2000-07-07
PRIOR APPLICATION NUMBER: 60/225,270
PRIOR FILING DATE: 2000-08-14
PRIOR APPLICATION NUMBER: 60/251,869
PRIOR FILING DATE: 2000-12-08
PRIOR APPLICATION NUMBER: 60/235,834
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: 60/234,274
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: 60/234,223
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: 60/228,924
PRIOR FILING DATE: 2000-08-30
PRIOR APPLICATION NUMBER: 60/224,518
PRIOR FILING DATE: 2000-08-14
PRIOR APPLICATION NUMBER: 60/236,369
PRIOR FILING DATE: 2000-09-29
PRIOR APPLICATION NUMBER: 60/224,519
PRIOR FILING DATE: 2000-08-14
PRIOR APPLICATION NUMBER: 60/220,964
PRIOR FILING DATE: 2000-07-26
PRIOR APPLICATION NUMBER: 60/241,809
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/249,299
PRIOR FILING DATE: 2000-11-17
PRIOR APPLICATION NUMBER: 60/236,327
PRIOR FILING DATE: 2000-09-29
PRIOR APPLICATION NUMBER: 60/241,785
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/244,617
PRIOR FILING DATE: 2000-11-01
PRIOR APPLICATION NUMBER: 60/225,268
PRIOR FILING DATE: 2000-08-14
PRIOR APPLICATION NUMBER: 60/236,368

PRIOR FILING DATE: 2000-09-29
PRIOR APPLICATION NUMBER: 60/251,856
PRIOR FILING DATE: 2000-12-08
PRIOR APPLICATION NUMBER: 60/251,868
PRIOR FILING DATE: 2000-12-08
PRIOR APPLICATION NUMBER: 60/229,344
PRIOR FILING DATE: 2000-09-01
PRIOR APPLICATION NUMBER: 60/234,997
PRIOR FILING DATE: 2000-09-25
PRIOR APPLICATION NUMBER: 60/229,343
PRIOR FILING DATE: 2000-09-01
PRIOR APPLICATION NUMBER: 60/229,345
PRIOR FILING DATE: 2000-09-01
PRIOR APPLICATION NUMBER: 60/229,287
PRIOR FILING DATE: 2000-09-01
PRIOR APPLICATION NUMBER: 60/229,513
PRIOR FILING DATE: 2000-09-05
PRIOR APPLICATION NUMBER: 60/231,413
PRIOR FILING DATE: 2000-09-08
PRIOR APPLICATION NUMBER: 60/229,509
PRIOR FILING DATE: 2000-09-05
PRIOR APPLICATION NUMBER: 60/236,367
PRIOR FILING DATE: 2000-09-29
PRIOR APPLICATION NUMBER: 60/237,039
PRIOR FILING DATE: 2000-10-02
PRIOR APPLICATION NUMBER: 60/237,038
PRIOR FILING DATE: 2000-10-02
PRIOR APPLICATION NUMBER: 60/236,370
PRIOR FILING DATE: 2000-09-29
PRIOR APPLICATION NUMBER: 60/236,802
PRIOR FILING DATE: 2000-10-02
PRIOR APPLICATION NUMBER: 60/237,037
PRIOR FILING DATE: 2000-10-02
PRIOR APPLICATION NUMBER: 60/237,040
PRIOR FILING DATE: 2000-10-02
PRIOR APPLICATION NUMBER: 60/240,960
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/239,935
PRIOR FILING DATE: 2000-10-13
PRIOR APPLICATION NUMBER: 60/239,937
PRIOR FILING DATE: 2000-10-13
PRIOR APPLICATION NUMBER: 60/241,787
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/246,474
PRIOR FILING DATE: 2000-11-08
PRIOR APPLICATION NUMBER: 60/246,532
PRIOR FILING DATE: 2000-11-08
PRIOR APPLICATION NUMBER: 60/249,216
PRIOR FILING DATE: 2000-11-17
PRIOR APPLICATION NUMBER: 60/249,210
PRIOR FILING DATE: 2000-11-17
PRIOR APPLICATION NUMBER: 60/226,681
PRIOR FILING DATE: 2000-08-22
PRIOR APPLICATION NUMBER: 60/225,759
PRIOR FILING DATE: 2000-08-14
PRIOR APPLICATION NUMBER: 60/225,213
PRIOR FILING DATE: 2000-08-14
PRIOR APPLICATION NUMBER: 60/227,182
PRIOR FILING DATE: 2000-08-22
PRIOR APPLICATION NUMBER: 60/225,214
PRIOR FILING DATE: 2000-08-14
PRIOR APPLICATION NUMBER: 60/235,836
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: 60/230,438
PRIOR FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/215,135
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: 60/225,266
PRIOR FILING DATE: 2000-08-14
PRIOR APPLICATION NUMBER: 60/249,218
PRIOR FILING DATE: 2000-11-17
PRIOR APPLICATION NUMBER: 60/249,208
PRIOR FILING DATE: 2000-11-17

PRIOR APPLICATION NUMBER: 60/249,213
PRIOR FILING DATE: 2000-11-17
PRIOR APPLICATION NUMBER: 60/249,212
PRIOR FILING DATE: 2000-11-17
PRIOR APPLICATION NUMBER: 60/249,207
PRIOR FILING DATE: 2000-11-17
PRIOR APPLICATION NUMBER: 60/249,245
PRIOR FILING DATE: 2000-11-17
PRIOR APPLICATION NUMBER: 60/249,244
PRIOR FILING DATE: 2000-11-17
PRIOR APPLICATION NUMBER: 60/249,217
PRIOR FILING DATE: 2000-11-17
PRIOR APPLICATION NUMBER: 60/249,211
PRIOR FILING DATE: 2000-11-17
PRIOR APPLICATION NUMBER: 60/249,215
PRIOR FILING DATE: 2000-11-17
PRIOR APPLICATION NUMBER: 60/249,264
PRIOR FILING DATE: 2000-11-17
PRIOR APPLICATION NUMBER: 60/249,214
PRIOR FILING DATE: 2000-11-17
PRIOR APPLICATION NUMBER: 60/249,297
PRIOR FILING DATE: 2000-11-17
PRIOR APPLICATION NUMBER: 60/232,400
PRIOR FILING DATE: 2000-09-14
PRIOR APPLICATION NUMBER: 60/231,242
PRIOR FILING DATE: 2000-09-08
PRIOR APPLICATION NUMBER: 60/232,081
PRIOR FILING DATE: 2000-09-08
PRIOR APPLICATION NUMBER: 60/232,080
PRIOR FILING DATE: 2000-09-08
PRIOR APPLICATION NUMBER: 60/231,414
PRIOR FILING DATE: 2000-09-08
PRIOR APPLICATION NUMBER: 60/231,244
PRIOR FILING DATE: 2000-09-08
PRIOR APPLICATION NUMBER: 60/233,064
PRIOR FILING DATE: 2000-09-14
PRIOR APPLICATION NUMBER: 60/233,063
PRIOR FILING DATE: 2000-09-14
PRIOR APPLICATION NUMBER: 60/232,397
PRIOR FILING DATE: 2000-09-14
PRIOR APPLICATION NUMBER: 60/232,399
PRIOR FILING DATE: 2000-09-14
PRIOR APPLICATION NUMBER: 60/232,401
PRIOR FILING DATE: 2000-09-14
PRIOR APPLICATION NUMBER: 60/241,808
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/241,826
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/241,786
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/241,221
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/246,475
PRIOR FILING DATE: 2000-11-08
PRIOR APPLICATION NUMBER: 60/231,243
PRIOR FILING DATE: 2000-09-08

Alignment Scores:

Pred. No.:	94.4	Length:	24173
Score:	10.00	Matches:	10
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	3.12%	Indels:	0
DB:	14	Gaps:	0

US-10-617-835-4 (1-320) x US-10-091-572-855 (1-24173)

QY 140 GlySerGlySerArgSerLeuGlyLeu 149

DB 19606 GGCTCAGGCTCCAGGTCTCCCTGGGCTT 19635

RESULT 10
US-10-437-963-48432/c

Sequence 48432, Application US/10437963
Publication NO. US20040123343A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Bardazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 48432
LENGTH: 420
TYPE: DNA
ORGANISM: Oryza sativa
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT4530_51107C.1
US-10-437-963-48432

Alignment Scores:

Pred. No.:	26	Length:	420
Score:	9.00	Matches:	9
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	2.81%	Indels:	0
DB:	19	Gaps:	0

US-10-617-835-4 (1-320) x US-10-437-963-48432 (1-420)

QY 41 ValAlaAlaSerAlaArgAlaAlaVal 49

DB 401 GTGGCAGCTCGGCTAGGGCGGGGTG 375

RESULT 11

US-10-425-115-122322/c
Sequence 122322, Application US/10425115
Publication No. US20040214272A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(53222)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 122322
LENGTH: 463
TYPE: DNA
ORGANISM: Zea mays
FEATURE:
OTHER INFORMATION: Clone ID: MRT4577_43041C.1
US-10-425-115-122322

Alignment Scores:

Pred. No.:	28.4	Length:	463
Score:	9.00	Matches:	9
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	2.81%	Indels:	0
DB:	20	Gaps:	0

US-10-617-835-4 (1-320) x US-10-425-115-122322 (1-463)

QY 40 LeuValAlaAlaSerAlaArgAlaAla 48

```
Db          442 CTTGTTGCTGCCAGTGTCCGCCGCGC 416
|||||
RESULT 12
US-10-425-115-137587
; Sequence 137587, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 137587
; LENGTH: 530
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(530)
; OTHER INFORMATION: unsure at all n locations
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_56958C.1
US-10-425-115-137587

Alignment Scores:
Pred. No.:      32.1      Length:      530
Score:          9.00      Matches:      9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match:    2.81%      Indels:      0
DB:             20        Gaps:         0

US-10-617-835-4 (1-320) x US-10-425-115-137587 (1-530)

Oy          158 ArgAngluThrlleuThrThraAspPro 166
|||||
Db          239 AGGAACGAACCTCACCACGAATCC 265

RESULT 13
US-09-823-245A-481/C
; Sequence 481, Application US/09823245A
; Publication No. US20020039760A1
; GENERAL INFORMATION:
; APPLICANT: Wong, Gordon G.
; APPLICANT: Clark, Hilary
; APPLICANT: Fechtel, Kim
; APPLICANT: Agostino, Michael J.
; APPLICANT: Howes, Steven H.
; APPLICANT: Resnick, Richard J.
; APPLICANT: Gulukota, Kamalakara
; APPLICANT: Graham, James R.
; APPLICANT: Genetics Institute, Inc.
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL SECRETED PROTEINS
; FILE REFERENCE: GIN 6401
; CURRENT APPLICATION NUMBER: US/09/823,245A
; CURRENT FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: 60/194,941
; PRIOR FILING DATE: 2000-04-06
; NUMBER OF SEQ ID NOS: 631
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 481
; LENGTH: 2849
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-823-245A-481

Alignment Scores:
```

```

Pred. No.:      147      Length:      2849
Score:          9.00      Matches:      9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match:    2.81%      Indels:      0
DB:             9        Gaps:         0

US-10-617-835-4 (1-320) x US-09-823-245A-481 (1-2849)

Oy          140 GlySerGlySerArgSerSerLeuGly 148
|||||
Db          1123 GGCTCTGGGTACGCTCTCTCTCGGA 1097

RESULT 14
US-10-311-455-122/C
; Sequence 122, Application US/10311455
; Publication No. US20030143606A1
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
; APPLICANT: PIEPENBROCK, Christian
; APPLICANT: BERLIN, Kurt
; TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Determ
; TITLE OF INVENTION: cytosine methylation
; FILE REFERENCE: 5013.1014
; CURRENT APPLICATION NUMBER: US/10/311,455
; CURRENT FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: PCT/EP01/07537
; PRIOR FILING DATE: 2001-07-02
; PRIOR APPLICATION NUMBER: DE 10032529.7
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DE 10043826.1
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 2424
; SEQ ID NO 122
; LENGTH: 12705
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 5677..5678
; OTHER INFORMATION: n is a or g or c or t
US-10-311-455-122

Alignment Scores:
Pred. No.:      572      Length:      12705
Score:          9.00      Matches:      9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match:    2.81%      Indels:      0
DB:             15        Gaps:         0

US-10-617-835-4 (1-320) x US-10-311-455-122 (1-12705)

Oy          239 LeuLeuIleIysProIysThrAsnAla 247
|||||
Db          286 TTACTAATATAAACCGAAACCAACGCGC 260

RESULT 15
US-10-311-455-386/C
; Sequence 386, Application US/10311455
; Publication No. US20030143606A1
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
; APPLICANT: PIEPENBROCK, Christian
; APPLICANT: BERLIN, Kurt
; TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Determ
; TITLE OF INVENTION: cytosine methylation
; FILE REFERENCE: 5013.1014
; CURRENT APPLICATION NUMBER: US/10/311,455
; CURRENT FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: PCT/EP01/07537
```

```

; PRIOR FILING DATE: 2001-07-02
; PRIOR APPLICATION NUMBER: DE 10032529.7
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DE 10043826.1
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 2424
; SEQ ID NO 388
; LENGTH: 16720
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-311-455-388

```

```

Alignment Scores:
Pred. No.: 733 Length: 16720
Score: 9.00 Matches: 9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.81% Indels: 0
DB: 15 Gaps: 0

```

US-10-617-835-4 (1-320) x US-10-311-455-388 (1-16720)

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QY 237 LYSLSYLSLEULLEULLEULYSAPROLYSTHR 245
DB 3994 AAAAACTACTATATTAAACCCAAACT 3968

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Search completed: August 19, 2005, 03:44:32
Job time : 684 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame_plus.p2n model

Run on: August 19, 2005, 00:57:16 ; Search time 3360 Seconds
(without alignments)
3625.169 Million cell updates/sec

Title: US-10-617-835-4

Perfect score: 320

Sequence: 1 MRALLPILPILSVFILSACG.....SHEGYGSDENVRHROGQP 320

Scoring table:

OLIGO
Xgapop 60.0 , Xgapext 60.0
Ygapop 60.0 , Ygapext 60.0
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 34239544 seqs, 19032134700 residues

Word size: 1

Total number of hits satisfying chosen parameters: 68477535

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Command line parameters:

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-O/cgn2.1/USPTO.spool.p/US10617835/rnat.18082005.115731.8758/app.query.fasta_1.519
-DB=EST -OFMT=fasta -SUFFIX=p2noligo.rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=oligo -TRANS=human0.cdi -LIST=45
-DOCLIGN=200 -THR.SCORE=quality -THR.MIN=1 -ALIGN=15 -MODE=LOCAL -OUTFMT=psio
-NORMext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US10617835 @CEN 1.1.5180 @rnat.18082005.115731.8758 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEX=7

Database :

EST:
1: gb_est1:*
2: gb_est2:*
3: gb_hic:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gsa1:*
9: gb_gsa2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	10	3.1	320	5 BX554222	BX554222 BX554222
2	10	3.1	491	1 AI332340	AI332340 GQ08A04.x
3	10	3.1	528	2 AM005450	AM005450 w286f05.x
4	10	3.1	576	6 CD65737	CD65737 f827c12.y
5	10	3.1	581	1 AI140766	AI140766 q850g02.x
6	9	2.8	254	1 AV326428	AV326428 AV326428
7	9	2.8	254	2 BB557704	BB557704 BB557704
8	9	2.8	404	2 BE092500	BE092500 IL2-BT073
9	9	2.8	441	2 BE434548	BE434548 EST405626

10	9	2.8	455	7	CN493609	MdFw2007k
11	9	2.8	464	5	BX091662	BX091662
12	9	2.8	479	2	AM037625	AM037625
13	9	2.8	485	7	CN284676	CN284676
14	9	2.8	486	1	AI897283	AI897283
15	9	2.8	518	1	AU282041	AU282041
16	9	2.8	525	5	BQ397697	BQ397697
17	9	2.8	528	1	AI486883	AI486883
18	9	2.8	530	8	AO663550	AO663550
19	9	2.8	543	1	AL779961	AL779961
20	9	2.8	554	6	CB87884	CB87884
21	9	2.8	572	6	CD290097	CD290097
22	9	2.8	575	6	CD319107	CD319107
23	9	2.8	595	5	BQ391883	BQ391883
24	9	2.8	621	5	BQ392079	BQ392079
25	9	2.8	619	4	BG721864	BG721864
26	9	2.8	625	5	BQ391914	BQ391914
27	9	2.8	630	9	CM505798	CM505798
28	9	2.8	640	4	BG129256	BG129256
29	9	2.8	654	8	AZ572177	AZ572177
30	9	2.8	664	6	CA148027	CA148027
31	9	2.8	676	9	BX970295	BX970295
32	9	2.8	687	9	CE516457	CE516457
33	9	2.8	702	6	CA147234	CA147234
34	9	2.8	711	8	BZ395507	BZ395507
35	9	2.8	747	9	CC923197	CC923197
36	9	2.8	769	9	CR215897	CR215897
37	9	2.8	784	5	BX316817	BX316817
38	9	2.8	793	6	CB621811	CB621811
39	9	2.8	805	6	CB619684	CB619684
40	9	2.8	814	7	CF220972	CF220972
41	9	2.8	818	7	CK288538	CK288538
42	9	2.8	829	9	CC518011	CC518011
43	9	2.8	851	7	CK298583	CK298583
44	9	2.8	872	9	CL795658	CL795658
45	9	2.8	901	9	CG216003	CG216003

ALIGNMENTS

RESULT 1
BX554222
LOCUS
DERIVATION
BX554222 Glosina moritans moritans adult infected gut Glosina moritans moritans CDNA clone Tbe14D05.q1c, mRNA sequence.

ACCESSION
BX554222
VERSION
BX554222.1 GI:33378317

KEYWORDS
SOURCE

ORGANISM
Glosina moritans moritans

REFERENCE
1 (bases 1 to 320)

AUTHORS
Lehane, M.J., Aksoy, S., Gibson, W., Keshornou, A., Berriman, M., Hamilton, J., Soares, M.B., Bonaldo, M.F., Lehane, S. and Hall, N.

TITLE
Adult midgut expressed sequence tags from the tsetse fly Glosina moritans moritans and expression analysis of putative immune response genes

JOURNAL
Genome Biol. 4 (10), R63 (2003)

MEDLINE
22881942

PUBMED
14519198

COMMENT
Contact: Hall N

Pathogen Sequencing Unit

The Sanger Institute The Wellcome Trust Genome Campus

Hinxton, Cambridge, CB10 1SA, UK

Request for clones, please contact: Mike Lehane

Prof. M.J. Lehane

School of Biological Sciences,

University of Wales,

Bangor LL57 2UW

All clones with suffix q1c are reverse primer reads starting at 5'

end of the cDNA all plc reads are from

Query Match: 3.12% Indels: 0
DB: 2 Gaps: 0

US-10-617-835-4 (1-320) x AW005450 (1-528)

Qy 140 Glycerglyserargserleucglyleu 149
DB 474 GGCTCAGGCTCCAGGTCCTCCTGGGCGCTT 445

RESULT 4
LOCUS CD675737 576 bp mRNA linear EST 24-JUN-2003
DEFINITION f827c12.y1 Human lens cDNA (Normalized): fs Homo sapiens cDNA clone
ACCESSION CD675737
VERSION CD675737.1 GI:32177468
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 576)
Wistow,G., Bernstein,S.L., Wyatt,M.K., Behal,A., Touchman,J.W., Bouffard,G., Smith,D. and Peterson,K.
Expressed sequence tag analysis of adult human lens for the NEIBank Project: over 2000 non-redundant transcripts, novel genes and splice variants
Mol. Vis. 8 (4), 171-184 (2002)
22103463
JOURNAL MEDLINE
PUBMED 12107413

COMMENT Contact: Wistow G
Section on Molecular Structure and Function
National Eye Institute
6/31, NIH, Bethesda, MD 20892-2740, USA
Tel: 301 402 3452
Fax: 301 496 0078
Email: graham@nei.nih.gov
Plate: 27 row: C column: 12
Seq primer: M13RP1 reverse primer (ABI).
Location/Qualifiers
source
1..576
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="f827c12"
/issue_type="Lens"
/dev_stage="Adult"
/lab_host="EMDH10B"
/clone_lib="Human Lens cDNA (Normalized): fs"
/note="Organ: Eye; Vector: pCMVSPORT6; A human lens library (by) was normalized by self-subtraction. One portion of double stranded plasmid DNA representing the library was linearized by NotI. This NotI digested library was used as a template for biotinylated DNA synthesis using SP6 RNA polymerase. Another portion of the double stranded plasmid library was converted to single-stranded circles in vitro using Gene II and Exonuclease III (Life Technologies). Single-stranded DNA (1 mg) was hybridized (Cot 500) with 41 mg of Bio-RNA and vector blocking oligonucleotides. The hybridized Bio-RNA/ss-circles were removed by streptavidin:phenol extraction. EST analysis was performed on the library at the NIH Intramural Sequencing Center (NISC)."

ALIGNMENT SCORES:
Pred. No.: 32.6 Length: 576
Score: 10.00 Matches: 10
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.12% Indels: 0
DB: 6 Gaps: 0

US-10-617-835-4 (1-320) x CD675737 (1-576)

Qy 140 Glycerglyserargserleucglyleu 149
DB 484 GGCTCAGGCTCCAGGTCCTCCTGGGCGCTT 513

RESULT 5
LOCUS A1140766/c 581 bp mRNA linear EST 05-OCT-1998
DEFINITION q450g02.x1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:1690226
ACCESSION A1140766
VERSION A1140766.1 GI:3648223
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 581)
NCI-CCAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
Unpublished (1997)
JOURNAL COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapb-rc@mail.nih.gov
This clone is available royalty-free through LINTL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 782 Std Error: 0.00
Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 444.
Location/Qualifiers
source
1..581
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1690226"
/issue_type="Pooled human melanocyte, fetal heart, and pregnant uterus"
/lab_host="DH10B"
/clone_lib="Soares_NHMPu_S1"
/note="Organ: mixed (see below); Vector: p7T73D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; Equal amounts of plasmid DNA from three NBHPU, and fetal heart NBH19W, were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 260232-265223, 340488-345479, and 484488-489479."

ALIGNMENT SCORES:
Pred. No.: 32.9 Length: 581
Score: 10.00 Matches: 10
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.12% Indels: 0
DB: 1 Gaps: 0

US-10-617-835-4 (1-320) x A1140766 (1-581)

Qy 140 Glycerglyserargserleucglyleu 149
DB 478 GGCTCAGGCTCCAGGTCCTCCTGGGCGCTT 449

RESULT 6
LOCUS AV326428/c 254 bp mRNA linear EST 11-NOV-1999
DEFINITION AV326428 RIKEN full-length enriched, adult male medulla oblongata Mus musculus cDNA clone 6330411A18 3' similar to AF009513 Mus musculus hematopoietic lineage switch 2 (HLS2) mRNA, mRNA sequence.


```

/db_xref="taxon:10090"
/clone="E330030E10"
/sex="female"
/tissue_type="ovary"
/dev_stage="2 days pregnant adult"
/lab_host="DH10B"
/clone_lib="RIKEN full-length enriched, 2 days pregnant
adult female ovary"
/note="Site 1: SalI; Site 2: BamHI; cDNA library was
prepared and sequenced in Mouse Genome Encyclopedia
Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in
RIKEN, Division of Experimental Animal Research in Riken
contributed to prepare mouse tissues. 1st strand cDNA was
primed with a primer 15'
GAGAGAGAGAGCGCGCGCAACTCGAGTTTCTTTTCTTTTCTTTVN 3'. cDNA was
prepared by using trehalose thermo-activated reverse
transcriptase and subsequently enriched for full-length by
cap-trapper. Second strand cDNA was prepared with the
primer adapter of sequence [5'
GAGAGAGAGATTCTGAGTTATTAATTAATCCCGCCCCCCCC 3']. cDNA
was cleaved with BamHI and XhoI. Vector: a modified
pBluescript KS(+) after bulk excision from Lambda FIC I."

```

ORIGIN

```

Alignment Scores:
Pred. No.: 150 Length: 254
Score: 9.00 Matches: 9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.81% Indels: 0
DB: Gaps: 0

```

US-10-617-835-4 (1-320) x BB557704 (1-254)

Oy 252 Tyrlvsgluasnyralaleutrmec 260
 Db 128 TATTAAGAAACTATGCTGTGATG 102

RESULT 8 BE092500 404 bp mRNA linear EST 12-JUN-2000
 LOCUS IL2-BT0734-260400-078-C08 BT0734 Homo sapiens cDNA, mRNA sequence.
 DEFINITION BE092500
 ACCESSION BE092500.1 GI:9482861
 VERSION EST.
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 404)
 Dlas Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M. R.,
 Nagai, M. A., da Silva, W. Jr., Zago, M. A., Bordin, S., Costa, F. F.,
 Goldman, G. H., Carvalho, A. F., Matsukuma, A., Bala, G. S., Simpson, D. H.,
 Brunstein, A., de Oliveira, P. S., Bucher, P., Jongeneel, C. V.,
 O'Hare, M. J., Soares, F., Brentani, R. R., Reis, L. F., de Souza, S. J. and
 Simpson, A. J.

REFERENCE

AUTHORS
 TITLE Shotgun sequencing of the human transcriptome with ORF expressed
 sequence tags
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
 MEDLINE 20202663
 PUBMED 10737800

COMMENT

CONTACT: Simpson A.J.G.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
 Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br
 This sequence was derived from the FAPESP/LICR Human Cancer Genome
 Project. This entry can be seen in the following URL
 (http://www.ludwig.org.br/scripts/gethtml2.pl?l=at2=il2-BT0734-260

```

400-078-C08&t3=2000-04-26&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 399.
Location/Qualifiers
1..404
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="BT0734"
/note="Organ: breast; Vector: puc18; Site 1: SmaI; Site 2:
SmaI; A mini-library was made by cloning products derived
from ORESTES PCR (U.S. Letters Patent application No.
196,716 - Ludwig Institute for Cancer Research) profiles
into the pUC 18 vector. Reverse transcription of tissue
mRNA and cDNA amplification were performed under low
stringency conditions."

```

ORIGIN

```

Alignment Scores:
Pred. No.: 232 Length: 404
Score: 9.00 Matches: 9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.81% Indels: 0
DB: Gaps: 0

```

US-10-617-835-4 (1-320) x BE092500 (1-404)

Oy 194 Aeptrhpaapvalphei1easnl1eap 202
 Db 258 GATACGACGCTTCTATTAACATCGAC 284

RESULT 9 BE34548 441 bp mRNA linear EST 18-MAY-2001
 LOCUS BE34548
 DEFINITION EST405626 tomato breaker fruit, TIGR Lycopersicon esculentum cDNA
 clone CLEG17N1, mRNA sequence.
 ACCESSION BE34548
 VERSION BE34548.1 GI:9432391
 KEYWORDS
 SOURCE Lycopersicon esculentum (tomato)
 ORGANISM
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 asterids; lamids; Solanales; Solanaceae; Solanum; Lycopersicon.
 1 (bases 1 to 441)
 Liang, F., Hansen, T. S., Craven, M. B., Bowman, C. L., Romling, C. M.,
 Niemman, W., Frazer, C. M., Martin, G. B., Giovannoni, J. J. and
 Tanksley, S. D.

REFERENCE

AUTHORS
 TITLE Generation of ESTs from tomato fruit tissue, breaker stage
 JOURNAL Unpublished (2000)
 COMMENT
 CONTACT: CUGI
 Clemson University Genomics Institute
 100 Jordan Hall, Clemson, SC 29634, USA
 Email: http://www.genome.clemson.edu/orders/index.html
 5 prime sequence.
 Location/Qualifiers
 1..441
 /organism="Lycopersicon esculentum"
 /mol_type="mRNA"
 /cultivar="T496"
 /db_xref="taxon:4081"
 /clone="CLEG17N1"
 /tissue_type="Pericarp"
 /dev_stage="breaker"
 /lab_host="SOLR"
 /clone_lib="tomato breaker fruit, TIGR"
 /note="Vector: pBluescriptSMCdup1; Site 1: EcoRI;
 Site 2: XhoI; Fruit were harvested at the breaker stage
 (first sign of lycopen accumulation on the blossom end of

FEATURES

source

the fruit). Fruit were cut in half and the seeds and locules were discarded prior to freezing the pericarp."

ORIGIN

Alignment Scores:

Pred. No.:	251	Length:	441
Score:	9.00	Matches:	9
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	2.81%	Indels:	0
DB:	2	Gaps:	0

US-10-617-835-4 (1-320) x BE434548 (1-441)

Oy 76 SerLeuThrgIyGIVAgTYrSerIle 84

DB 219 AGCTTGACCGGCGCCGATCTCCATC 193

RESULT 10

CN493609

LOCUS Mdfw2007k07.y1 Mdfw Malus x domestica cDNA clone Mdfw2007k07.5',
DEFINITION similar to SW:TL16,ARATH 022773 TRYPAKOID LUMENAL 16.5 KDA PROTEIN,
CHLOROPLAST PRECURSOR, mRNA sequence.

ACCESSION

CN493609

VERSION

CN493609.1

KEYWORDS

EST.

SOURCE

Malus x domestica (cultivated apple)

ORGANISM

Malus x domestica

REFERENCE

Alwinckle,H., Mainio,M., Carroll,N., Goldbrogh,P., Ovis,K.,
Clifton,S., Pape,D., Marra,M., Hillier,L., Martin,J., Wylie,T.,
Dante,M., Theising,B., Bowers,Y., Gibbons,M., Ritzer,E., Ronko,I.,
Tsegareishvili,R., Kennedy,S., Waterston,R. and Wilson,R.
Apple Functional Genomics grant - NSF 0321702
Unpublished (2004)

AUTHORS

Korban,S., Vokhin,L., Liu,L., Gasic,K., Gonzales,O., Hernandez,A.,
Alwinckle,H., Mainio,M., Carroll,N., Goldbrogh,P., Ovis,K.,
Clifton,S., Pape,D., Marra,M., Hillier,L., Martin,J., Wylie,T.,
Dante,M., Theising,B., Bowers,Y., Gibbons,M., Ritzer,E., Ronko,I.,
Tsegareishvili,R., Kennedy,S., Waterston,R. and Wilson,R.
Apple Functional Genomics grant - NSF 0321702
Unpublished (2004)

TITLE

Apple Functional Genomics grant - NSF 0321702

JOURNAL

Unpublished (2004)

COMMENT

Contact: Schuyler S. Korban
Apple Functional Genomics grant - NSF 0321702
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
Library materials provided by: Schuyler S. Korban Library
constructed by: A. Hernandez / K. Gasic Library sequenced by:
Washington University Genome Sequencing Center
Washu EST name: aaf25f04.y1.

FEATURES

location/Qualifiers

SOURCE

1..455

ORGANISM

Malus x domestica

MOIETY

mol_type="mRNA"

LABORATORY

clone="Mdfw2007k07"

CLONE

lab_host="DH10B ampicillin resistant"

CLONE

clone_lib="Mdfw"

NOTE

/note="Vector: DH10B ampicillin resistant; Site 1: NotI;
Site 2: EcoRI; Total RNA was extracted separately from
each stage (bud, balloon, open and after pollination),
using the 'pine tree' method. Poly(A)+mRNA was isolated
twice from total RNA from each stage using the Qiagen
Direct mRNA kit (Qiagen). mRNA was reverse transcribed
into double stranded cDNA using a modified oligo18(dT)
primer with an identifying tag sequence (see table below).
cDNAs from different stages were pooled in equal amounts
before adaptor ligation. Tag identification when
sequencing from 5' end: Stage 1 (bud) insert 18(A)TCGA;
Stage 2 (balloon) insert 18(A)TCGA; Stage 3 (open) insert
18(A)TCGT; Stage 4 (after pollination) insert 18(A)TCGT.
Tag identification when sequencing from 3' end: Stage 1

ORIGIN

Alignment Scores:

Pred. No.:	259	Length:	455
Score:	9.00	Matches:	9
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	2.81%	Indels:	0
DB:	7	Gaps:	0

US-10-617-835-4 (1-320) x CN493609 (1-455)

Oy

1 MeArGAlaargLeuIleProIle 9

DB

389 ATGAGACCAAGACTATTAATTCACATA 415

RESULT 11

EX091662/c

LOCUS

EX091662 Soares NFL T GBC S1 Homo sapiens cDNA clone

DEFINITION

IMAGE98E075157, IMAGE:2092014, mRNA sequence.

ACCESSION

EX091662

VERSION

EX091662.1

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

REFERENCE

1 (bases 1 to 464) Hennig,S., Neubert,P., Pertsch,E., Peters,M.,
Ebert,L., Heil,O., Schneider,D. and Korn,B.
Human Unigeneset - RZPD3
Human Unigeneset (2003)
Unpublished (2003)
Contact: Ina Rolfs
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Im Neuenheimer Feld 360, D-69120 Heidelberg, Germany
RZPD; IMAGE98E075157.
RZPDLIB; I.M.A.G.E. cDNA Clone Collection;
Human Unigeneset - RZPD3 (RZPDLIB No.972)
http://www.rzpd.de/CloneCards/cgi-
bin/showlib.pl.cgi/response?libNo=972 Contact: Ina Rolfs
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Heubnerweg 6, D-14059 Berlin, Germany

TITLE

Human Unigeneset - RZPD3

JOURNAL

Unpublished (2003)

COMMENT

Contact: Ina Rolfs

ORIGIN

US-10-617-835-4 (1-320) x CN493609 (1-455)

Oy

1 MeArGAlaargLeuIleProIle 9

DB

389 ATGAGACCAAGACTATTAATTCACATA 415

RESULT 11

EX091662/c

EX091662 Soares NFL T GBC S1 Homo sapiens cDNA clone

IMAGE98E075157, IMAGE:2092014, mRNA sequence.

EX091662

EX091662.1

EST.

Homo sapiens (human)

Homo sapiens

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

1 (bases 1 to 464) Hennig,S., Neubert,P., Pertsch,E., Peters,M.,
Ebert,L., Heil,O., Schneider,D. and Korn,B.
Human Unigeneset - RZPD3
Human Unigeneset (2003)
Unpublished (2003)
Contact: Ina Rolfs
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Im Neuenheimer Feld 360, D-69120 Heidelberg, Germany
RZPD; IMAGE98E075157.
RZPDLIB; I.M.A.G.E. cDNA Clone Collection;
Human Unigeneset - RZPD3 (RZPDLIB No.972)
http://www.rzpd.de/CloneCards/cgi-
bin/showlib.pl.cgi/response?libNo=972 Contact: Ina Rolfs
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Heubnerweg 6, D-14059 Berlin, Germany

Tel: +49 30 32639 101
Fax: +49 30 32639 111
www.rzpd.de

This clone is available royalty-free from RZPD;
contact RZPD (clone@rzpd.de) for further information. Seq primer:
M13r, Primer sequence: TTTCCACAGCAACAGCTATGAC.

FEATURES

SOURCE

1.464
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE8075157 ; IMAGE:2092014"
/lab_host="DH10B"
/clone_lib="Soares_NFL_T_GBC_S1"
/note="Organ: pooled; Vector: pT73D-Pac (Pharmacia) with
a modified polylinker; Site 1: Not I; Site 2: Eco RI;
Equal amounts of plasmid DNA from three normalized
libraries (fetal lung NBHL19W, testis NHT, and B-cell
NCI CGAP GC91) were mixed and as circles were made in
vitro. Following HAP purification, this DNA was used as
tracer in a subtractive hybridization reaction. The driver
was PCR-amplified cDNAs from pools of 5,000 clones made
from the same 3 libraries. The pools consisted of
I.M.A.G.E. clones 297480-302087, 682632-687239,
726408-728711, and 728096-731399. Subtraction by Bento
Soares and M. Fatima Bonaldó."

ORIGIN

Alignment Scores:

Pred. No.:	264	Length:	464
Score:	9.00	Matches:	9
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	2.81%	Indels:	0
DB:	5	Gaps:	0

US-10-617-835-4 (1-320) x BX091662 (1-464)

Qy 9 |||leupheservai|phei|leuser 17

Db 232 ATTCTTCTCTGTGTCATCTACTGCC 206

RESULT 12

AW037625/c

LOCUS EST179083 tomato mixed elictor, BTI Lycopersicon esculentum cDNA

DEFINITION clone cLET309, mRNA sequence.

ACCESSION AW037625

VERSION AW037625.1 GI:5896379

KEYWORDS EST.

ORGANISM Lycopersicon esculentum (tomato)

SOURCE Lycopersicon esculentum

EUKARYOTA; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Asteridae; lamiales; Solanales; Solanaceae; Solanum; Lycopersicon.

1 (bases 1 to 479)

D'Aacenzo, M., He, X., Lyman, J., Holt, I.E., Liang, F., Upton, J.,

Romling, C.M., Craven, M.B., Fujii, C.Y., Bowman, C.L., Nieman, W.,

Fraser, C.M., Venter, J.C., Martin, G.B., Tankale, S.D. and

Giovannoni, J.

Generation of ESTs from tomato leaf tissue

Unpublished (1999)

CONTACT: CUGI

Clemson University Genomics Institute

Clemson University

100 Jordan Hall, Clemson, SC 29634, USA

Email: <http://www.genome.clemson.edu/orders/index.html>

5 prime sequence.

Location/Qualifiers

1..479

/organism="Lycopersicon esculentum"

/mol_type="mRNA"

/cultivar="Rio Grande Ptor"

/db_xref="taxon:4081"

/clone="cLET309"

/tissue_type="leaf"

/dev_stage="4-6 week old plants"

/lab_host="XLI-Blue MRF"

/clone_lib="tomato mixed elictor, BTI"

/note="Vector: pBluescript SK(-); Site 1: EcoRI; Site 2:

XhoI; cLET - inoculated with a variety of disease response

elictors. Plants exposed to 2,6 dichloroisocitric

acid, BTH, jasmonic acid, ethylene, fenchon, Eix,

okadaic acid, or systemin prior to tissue harvest. EcoRI

site was destroyed during cloning."

ORIGIN

Alignment Scores:

Pred. No.:	271	Length:	479
Score:	9.00	Matches:	9
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	2.81%	Indels:	0
DB:	2	Gaps:	0

US-10-617-835-4 (1-320) x AW037625 (1-479)

Qy 76 Serleutnrglyg|yarg|tyrser|le 84

Db 152 AGCTTGACCGGCGCGACTCCATC 126

RESULT 13

CN284676/c

LOCUS CN284676 485 bp mRNA linear EST 16-MAY-2004

DEFINITION 17000531558899 GRN_ES Homo sapiens cDNA 5', mRNA sequence.

ACCESSION CN284676

VERSION CN284676.1 GI:47301090

KEYWORDS EST.

SOURCE Homo sapiens

ORGANISM Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

1 (bases 1 to 485)

Brandenberger, R., Wei, H., Zhang, S., Lei, S., Murage, J., Flak, G.J.,

Li, Y., Xu, C., Fang, R., Guejler, K., Rao, M.S., Mandalam, R.,

Lebkowski, J. and Stanton, L.W.

Transcriptome characterization elucidates signaling networks that

control human ES cell growth and differentiation

Nat. Biotechnol. 22 (6), 707-716 (2004)

Contact: Brandenberger R

Regenerative Medicine

Genon Corporation

230 Constitution Drive, Menlo Park, CA 94025, USA

Tel: 650 473 8658

Fax: 650 473 7760

Email: rbrandenberger@genon.com

Insert Length: 485 Std Error: 0.00.

Location/Qualifiers

1..485

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/tissue_type="embryonic stem cells, cell lines H1, H7, and

H9"

/clone_lib="GRN_ES"

/note="Oligo dT primed, full-length enriched cDNA library

from undifferentiated hES cell lines H1 (p32), H7 (p29),

and H9 (p26) maintained in feeder-free conditions"

Alignment Scores:

Pred. No.:	275	Length:	485
Score:	9.00	Matches:	9
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	2.81%	Indels:	0

DB: 7 Gaps: 0

US-10-617-835-4 (1-320) x CN284676 (1-485)

OY 140 G|Serg|ySerySergSer|en|y 148
 |||||
 DB 381 GGCTCTGGGTACGCTCCTCCCTGGGA 355

RESULT 14
 A1897283/c 486 bp mRNA linear EST 18-MAY-2001

LOCUS EST26642 tomato ovary, TAMU Lycopersicon esculentum cDNA clone

DEFINITION CLD26N1, mRNA sequence.

ACCESSION A1897283

VERSION A1897283.1 GI:5603101

KEYWORDS EST.

SOURCE Lycopersicon esculentum (tomato)

ORGANISM Lycopersicon esculentum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 asterids; lamids; Solanales; Solanaceae; Solanum; Lycopersicon.
 1 (bases 1 to 486)
 Alcalá, J., Vrebalov, J., White, R., Matern, A. L., Vision, T.,
 Holt, I. E., Liang, F., Upton, J., Romling, C. M., Craven, M. B.,
 Fujii, C. Y., Bowman, C. L., Niernan, W., Fraser, C. M., Venter, J. C.,
 Martin, G. B., Tanksley, S. D. and Giovannoni, J.
 Generation of ESTs from tomato carpel tissue
 Unpublished (1999)

TITLE JOURNAL

COMMENT Contact: CUGI
 Clemson University Genomics Institute
 Clemson University
 100 Jordan Hall, Clemson, SC 29634, USA
 Email: <http://www.genome.clemson.edu/orders/index.html>
 5 prime sequence.

FEATURES
 source
 Location/Qualifiers
 1..486
 /organism="Lycopersicon esculentum"
 /mol_type="mRNA"
 /cultivar="TA496"
 /db_xref="taxon:4081"
 /clone="CLD26N1"
 /tissue_type="carpel"
 /dev_stage="5 days pre-anthesis to 5 days post-anthesis"
 /lab_host="X11-Blue MRP"
 /clone_lib="tomato ovary, TAMU"
 /note="Vector: pBluescript SK(-); Site 1: EcoRI; Site 2:
 XhoI; cLED - Tomato Carpel EST Library. OligodT-primed and
 directionally cloned cDNA in vector lambda ZAP II with 5'
 and 3' ends located at the EcoRI and XhoI sites,
 respectively."

ORIGIN

Alignment Scores:

Pred. No.:	275	Length:	486
Score:	9.00	Matches:	9
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	2.81%	Indels:	0
DB:	1	Gaps:	0

US-10-617-835-4 (1-320) x A1897283 (1-486)

OY 76 SerLeuThrGlyGlyArgTyrSerIle 84
 |||||
 DB 266 AGCTTGACCGGCGCGATCTCCATC 240

RESULT 15
 A0282041 518 bp mRNA linear EST 03-DEC-2002

LOCUS A0282041 Molgula tectiformis library Molgula tectiformis cDNA clone

DEFINITION MT19B2G11T 3', mRNA sequence.

ACCESSION A0282041

VERSION A0282041.1 GI:26021539

KEYWORDS EST.

SOURCE Molgula tectiformis

ORGANISM Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea;
 Stolidobranchia; Molgulidae; Molgula.
 1 (bases 1 to 518)
 Takada, N., Murakami, S. D., Swalla, B. J. and Satch, N.
 EST analysis of tailless ascidian M. tectiformis
 Unpublished (2002)

TITLE JOURNAL

COMMENT Contact: Seiko D. Murakami
 Graduate School of Science, Department of Zoology
 Kyoto University
 Sakyo-ku, Kyoto 606-8502, Japan
 Tel: 81-75-753-4095
 Fax: 81-75-705-1113
 Email: seiko@ascidian.zool.kyoto-u.ac.jp.

FEATURES
 source
 Location/Qualifiers
 1..518
 /organism="Molgula tectiformis"
 /mol_type="mRNA"
 /db_xref="taxon:30286"
 /clone="MT19B2G11T"
 /clone_lib="Molgula tectiformis library"

ORIGIN

Alignment Scores:

Pred. No.:	292	Length:	518
Score:	9.00	Matches:	9
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	2.81%	Indels:	0
DB:	1	Gaps:	0

US-10-617-835-4 (1-320) x A0282041 (1-518)

OY 169 ThrAlaPheLeuSerHisIleuValGln 177
 |||||
 DB 391 ACTGCTTCTCTCTGCACTCGTCCAG 417

Search completed: August 19, 2005, 02:17:54
 Job time : 3378 secs


```

FT      CDS      /tag= 9
FT      CDS      583..1545
FT      CDS      /*tag= h
FT      CDS      /label= Oref1
FT      RBS      1573..1579
FT      CDS      /*tag= 1
FT      CDS      1585..3114
FT      CDS      /*tag= j
FT      CDS      /label= OrefB
XX      DE19534579-A1.
XX      20-MAR-1997.
XX      18-SEP-1995; 95DE-01034579.
XX      18-SEP-1995; 95DE-01034579.
XX      (PLAC ) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
XX      WPI; 1997-180942/17.
XX      DR P-PSDB; AAM18784, AAM18785, AAM18786.
XX      PT Nucleic acids encoding Neisseria adhesion proteins - for therapeutic and
XX      PS diagnostic use.
XX      Claim 1; Page 11-13; 20pp; German.
XX      CC OrlA and OrlB in complexes with the protein PilC are capable of adhering
XX      CC to human cells. Products obtained from the DNA are useful in medicaments,
XX      CC diagnostic compns. and vaccines, esp. for treatment of Neisseria
XX      CC gonorrhoeae and N. meningitidis infections
XX      SQ Sequence 3287 BP; 1016 A; 741 C; 752 G; 778 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 0 Length: 3287
Score: 320.00 Matches: 320
Percent Similarity: 100.00% Conservative: 0
Best local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-10-617-835-4 (1-320) x AAT70386 (1-3287)
OY      1 MetArg1AAArgLeuLeu11Pro11LeuPheSerValPhe11LeuSerAlaCysGly 20
DB      583 ATGCGGCGACGGCTGCTGATACCTATTCCTTTTCGTTTATTTTATCCGCTCGCGG 642
OY      21 ThrLeuThrgIy11eProSerH1eGly1y1y1ySArqPhea1aVal1GluGln1uLeu 40
DB      643 ACACGTGACAGGTATTCATCGCATGCGGAGCAAGCCTTCGCGGTGAAACAAGACTT 702
OY      41 Val1a1a1aSer1a1a1aGAla1aVal1y1y1ySArqPhea1aVal1GluGln1uLeu 60
DB      703 GTGGCCGCTTCTGCACAGCTGCGGTTAAACATGATTTTACAGGCATTACAGGAGA 762
OY      61 LysVal1a1eLeuYr11eAla1aThrMeG1y1y1ySArqPhea1aVal1GluGln1uLeu 80
DB      763 AAAGTTGATTCATTCATTGCAACTATGCGCAACAGGATTACAGGAGTTTACAGGAG 822
OY      81 ArgTy1Ser11eAsp1a1eLeu11eArg1y1y1y1y1y1y1y1y1y1y1y1y1y1y1y 100
DB      823 CGCTACTCCATTGATGACGCTGATTGCGCGGCAATACATTAACAGGCTCGCGCAC 882
OY      101 AspTy1ThrTy1rProArgTy1y1y1y1y1y1y1y1y1y1y1y1y1y1y1y1y1y1y 120
DB      883 GATTACACCTATCCGCGTTACGAAACCAACCGCTGTAACCAATACAGGCGTTTACAGG 942
OY      121 LeuThrThrSer1eSerThrLeuAsn1a1Pro1a1eLeuSerArgThrGlnSerAspGly 140
DB      943 TTAACCACTTCTTATCTACACTTAATGCCCCCTGCACTCTCGCGCAACCAATCAGAG 1002

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OY      141 SerGlySerArgSerSerLeuGlyLeuAsn11eGly1y1y1y1y1y1y1y1y1y1y1y1y 160
DB      1003 AGCGGAAGTAGAACAAGCTGCTGGCTTAATTTGCGGGATGGGGATTTATCGAAATGAA 1062
OY      161 ThrLeuThrThraPProArgAspThrAlaPheLeuSerH1eLeuVal1GlnThyValPhe 180
DB      1063 ACCTTGACGACCAACCGCGGACACCTCTTCTTCCCACTTGTAACAACCGTATTT 1122
OY      181 PheLeuArgGly11eAspVal1a1SerPro1a1a1a1a1a1a1a1a1a1a1a1a1a1a1a 200
DB      1123 TTCCTGCGCGCATAGACGTTGTTTCTCTCCCAATCCCGATACAGATGTGTTATTTAAC 1182
OY      201 IleAspValPheGlyThr11eArgAsnArgThrGluMetH1eLeuTy1y1y1y1y1y1y 220
DB      1183 ATCGACGATTCGGAACGATACGCAACAGAACCGAAATGCACCTATACAAATGCCGAAACA 1242
OY      221 Leu1y1a1aGlnThr1y1y1y1y1y1y1y1y1y1y1y1y1y1y1y1y1y1y1y1y1y1y 240
DB      1243 CTGAAGCCCAACCAAACTGGAATATTTCCGAGTGAACAGAACCAATMAAAATGCTC 1302
OY      241 Ile1ySPPro1ySPThraPProArgAsn1a1a1a1a1a1a1a1a1a1a1a1a1a1a1a1a1a 260
DB      1303 ATCAAAACCCAAACCAATGCGTTTGAAGCTGCTTAAAGAAATTAACGCAATTGTGATG 1362
OY      261 GlyProTy1y1y1y1y1y1y1y1y1y1y1y1y1y1y1y1y1y1y1y1y1y1y1y1y 280
DB      1363 GGGCCGTATAAAGTAACCAAAAGAAATCAACCGACGGAAGGATTAATGCTGATTTCTCC 1422
OY      281 Asp11eArgProTy1y1y1y1y1y1y1y1y1y1y1y1y1y1y1y1y1y1y1y1y1y1y1y 300
DB      1423 GATATCCGCGCAATACGCAATCAATACGATGATCCCGCCCATCGTAAAGGCTGATTAAC 1482
OY      301 SerH1eGlnGlyTy1y1y1y1y1y1y1y1y1y1y1y1y1y1y1y1y1y1y1y1y1y1y1y 320
DB      1483 AGTCATGAGGGGTATGATACAGCGATGAGCACTGCGACACATACAAAGGCAACCT 1542

RESULT 2
ABZ37917
ID      ABZ37917 standard; DNA; 960 BP.
XX      XX
XX      AC      ABZ37917;
XX      DT      07-MAR-2003 (first entry)
XX      DE      N. gonorrhoeae nucleotide sequence SEQ ID 423.
XX      KW      Antibacterial; infection; vaccine; gene therapy; gene; ds.
XX      OS      Neisseria gonorrhoeae.
XX      PN      W0200279243-A2.
XX      PD      10-OCT-2002.
XX      PF      12-FEB-2002; 2002WO-1B002069.
XX      PR      12-FEB-2001; 2001GB-00003424.
XX      PA      (CHIR-) CHIRON SPA.
XX      PI      Fontana MR, Piza M, Maignani V, Monaci E;
XX      DR      WPI; 2003-058415/05.
XX      DR      P-PSDB; ABP76947.
XX      PT      New protein from Neisseria gonorrhoeae, useful for the manufacture of a
XX      PS      medicament for treating or preventing N. gonorrhoeae infection.
XX      CC      Disclosure; Page 220; 815pp; English.
XX      CC      The present invention relates to proteins from Neisseria gonorrhoeae.
XX      CC      Also disclosed are the nucleic acid molecules encoding the proteins and
XX      CC      antibodies that specifically bind to the proteins. The composition

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comprising the protein, nucleic acid or antibody is useful for the manufacture of a medicament for treating or preventing N. gonorrhoeae infection, this may be in the form of a vaccine or gene therapy.
 CC Sequences given in records AB237706-AB242016 represent nucleic acid molecules of the invention

XX Sequence 960 BP; 275 A; 241 C; 225 G; 219 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	1,21e-279	Length:	960
Score:	282.00	Matches:	319
Percent Similarity:	99.38%	Conservative:	0
Best Local Similarity:	99.38%	Mismatches:	1
Query Match:	88.12%	Indels:	2
DB:	10	Gaps:	0

US-10-617-835-4 (1-320) x AB237917 (1-960)

QY 1 MetATGAlaArgLeuLeuileProileuPheSerValPheileuSerAlaCysGly 20
 DB 1 ATGCGGGCAGCGCTGTATACCTATTCTTTTTCAGTTTATTATTATCCCGCTGCGG 60
 QY 21 ThrLeuThrGlyIleProSerHieGlyGlyIleArgPheAlaValGluGlnGluLeu 40
 DB 61 ACACGACAGGTATTCATCGCATGGCGGAGGCAACGCTTCGCGGTGCAACAGACTT 120
 QY 41 ValAlaIleSerAlaArgAlaAlaValIleYaaPheMetAepLeuGlnAlaLeuHieGlyArg 60
 DB 121 GTGGCGCGCTTCGCGAGACTCCGTTAAAGACATGAGATTTCAGGCATTACACGACGA 180
 QY 61 LysValAlaLeuTyrlleAlaThrMetGlyAaPngInGlySerGlySerLeuThrGlyGly 80
 DB 181 AAGAGTTGCACTTATTCAGTTCAGTATGGCGAGCAAGGTTTCAGGCACTTTCAGAGGGGT 240
 QY 81 ArgTySerIleAaPAlaLeuileArgGlyGlyIleAaSnSerProAlaValArgThr 100
 DB 241 CGCTACTCATTTGATGACACTGATTCGCGGCGAATACATAAACAGCCCTGCGCGAC 300
 QY 101 AapTyThrTyProArgTyGluThrThrAlaGluThrThSerGlyGlyLeuThrGly 120
 DB 301 GATTACACCTATCCGCTTACGAAACCAACCGCTGAACCAACATCAGCGCTTTCAGCGGT 360
 QY 121 LeuThrThrSerLeuSerThrleuAaSnAlaProAlaLeuSerArgThrGlnSerAaPng 140
 DB 361 TTAACTCACTTCTTTATCTACACTTAATGCCCCGCACTTCGCGACCCCAATCAGAGCT 420
 QY 141 SerGlySerArgSerSerLeuGlyLeuAaSnIleGlyGlyMetGlyAaPtyrArgAaGln 160
 DB 421 AGCGAAGTGAAGAGGAGCTGTGGCTTAATATTGGCGGAGATGGGGGATTATCGAATGA 480
 QY 161 ThrLeuThrThrAaPProArgAaPThrAlaPheLeuSerHieLeuValGlnThrValPhe 180
 DB 481 ACCTTGACGACCAACCCGCGGACACCTGCTTTCTTCCACTGTGTCAGACCGCTATT 540
 QY 181 PheLeuArgGlyIleAaPValIleSerProAlaAaSnAlaAaPThrAaPValPheIleAaSn 200
 DB 541 TTCCTCGCGGCGCATACAGCTTGTCTCTCCGCAATGCCGATACAGATGTGTTATTAC 600
 QY 201 IleAaPValPheGlyThrIleArgAaSnArgThrGluMetHieLeuTyrAaSnIleGluThr 220
 DB 601 ATCGACGTATTCGAAACGATACGCAACGAAACGAAATCAGCTATACATCCGGAACA 660
 QY 221 LeuIleValGlnThrIleLeuGluGlyIlePheAlaValAaPArgThrAaSnIleValLeuLeu 240
 DB 661 CTGAAGCCCAACCAAACTGGAATAATTCGACAGTACAGAACCAATTAATAATTCCTC 720
 QY 241 IleLeuPProIleThrAaSnAlaPheGlnIleAlaIleTyrlleGlyAaSnTyrlaLeuThrPmet 260
 DB 721 ATCAAAACCAAAACCAATCGTTTGAAGCTGCTATTAAGAAATTAATCCATTTGGATG 780
 QY 261 GlyProTyrlleValSerIleGlyIleTyProThrGlnGlyIleuMetValAaPheSer 280
 DB 781 GGGCGGTATTAAGTAAAGCAATCAAAACGACGAAAGATGATGATGATTCATTTCTCC 840

QY 281 AspIleArg-ProTyrlleAaSnHieThrGlyAaSnSerAlaProSerValGluAlaAaPAs 300

DB 841 GATATCCA-ACCATCGGCAATCATACGGGTACTCCGCCCATCCGATAGAGGCTGATTA 899

QY 300 nSerHieGluGlyTyrlleTySerAaPngIleAlaValArgGlnHieArgGlnGlyGlnr 320

DB 900 CAGTCATAGGGGCTATGATATACAGCATGAGCACTGCGACAACTATGACAAAGGCAACC 959

QY 320 Q 320

DB 960 T 960

RESULT 3

AA212008

ID AA212008 standard; DNA, 963 BP.

AC AA212008;

DT 08-OCT-1999 (first entry)

DE Neisseria gonorrhoeae complete ORF15 sequence.

KW Neisseria meningitidis; Neisseria gonorrhoeae; antigen; vaccine; treatment; Neisseria infection; meningitis; septicemia; gonorrhea; ss.

OS Neisseria gonorrhoeae.

PN WO924578-A2.

PD 20-MAY-1999.

PF 09-OCT-1998; 98WO-1B001665.

PR 06-NOV-1997; 97GB-00023516.

PR 14-NOV-1997; 97GB-00024190.

PR 27-NOV-1997; 97GB-00025158.

PR 10-DEC-1997; 97GB-00026147.

PR 14-JAN-1998; 98GB-00000759.

PR 01-SEP-1998; 98GB-00019016.

PA (CHIR-) CHIRON SPA.

PI Maignani V, Rappuoli R, Pizza M, Scarlato V, Grandi G;

DR WPI, 1999-327407/27.

XX P-PsDB; AAY38540.

PT Proteins from Neisseria meningitidis and N. gonorrhoeae useful for

PS diagnosis, treatment and prevention of infection.

PS Claim 9; Page 100; 524pp; English.

XX Nucleotide sequences AA211972-Z12358 represent open reading frames (ORFs) of Neisseria meningitidis and N. gonorrhoeae which encode antigenic proteins (see AAY38499-Y38944). The antigenic proteins, their fragments, their nucleic acids and antibodies are used for diagnosis, prevention (as vaccines) or treatment of Neisseria infections, such as meningitis, CC septicemia and gonorrhea. Both organisms are closely related. Fragments of the nucleic acids are useful as hybridisation probes and antisense reagents

XX Sequence 963 BP; 276 A; 241 C; 226 G; 220 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	1,21e-279	Length:	963
Score:	282.00	Matches:	319
Percent Similarity:	99.38%	Conservative:	0
Best Local Similarity:	99.38%	Mismatches:	1
Query Match:	88.12%	Indels:	2
DB:	2	Gaps:	0

US-10-617-835-4 (1-320) x AAZ54614 (1-963)

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QY      1 MetArgAlaArgLeuLeuIleProIleLeuPheSerValPheIleLeuSerAlaCysGly 20
Db      1 ATGGGGGACGCGCTGATACCTATCTTTTTCAGTTTATTTATTTATTCGCCGCCGCGGG 60
QY      21 ThrLeuThrGlyIleProSerHisGlyGlyIleYsArgPheAlaValGlyGlnGluLeu 40
Db      61 ACACAGACAGAGTATTCATCCGATGCGGAGGCAAAACCTTCGCGGTGCAACAGAACTT 120
QY      41 ValAlaAlaSerAlaArgAlaAlaValIleYsAspMetAspLeuGlnAlaLeuHisGlyArg 60
Db      121 GTGGCCGCTCTCGCCAGAGCTGCCGTAAAGACAATGATTTACAGGCACTTACCGCAAGA 180
QY      61 LysValAlaLeuYrIleAlaThrMetGlyAspGlnGlySerGlySerLeuThrGlyGly 80
Db      181 AAAGTTGATGTGATTCATTCGCAACTATGGGCGACCAAGGTTCAAGGAGTTTACAGGGGGGT 240
QY      81 ArgTyrSerIleAspAlaLeuIleArgGlyGlyIleAsnSerProAlaValArgThr 100
Db      241 CGCTACTCATTTGATGACCTGATTCGCCGCAATTCATTAACAGCCCTGCCGTCCGCACCC 300
QY      101 AspTyrThrTyrProArgTyrGlyThrThrAlaGluThrThrSerGlyGlyLeuThrGly 120
Db      301 GATTACACCTATCCGCGTTACGAAACCAACCCCTGAAACAAATCATCAGCGGTTGACGGGT 360
QY      121 LeuThrThrSerLeuSerThrLeuAsnAlaProAlaLeuSerArgThrGlnSerAspGly 140
Db      361 TTAAACCACTTCTTATTCATCACTTAATGCCCTGACCTCGCGACCAATCGACACCGT 420
QY      141 SerGlySerArgSerSerLeuGlyLeuAsnIleGlyIleMetGlyAspTyrArgAsnGlu 160
Db      421 AGCGGAAGTATGAGAGAGCTGGGCTTAATATTTGGCGGGATGGGGGATTAACGAATGAA 480
QY      161 ThrLeuThrThrAsnProArgAspThrAlaPheLeuSerHisLeuValGlnThrValPhe 180
Db      481 ACCTTGACGACCAACCCCGCGACACTGCTTCTTCTTCCACTGGTGCCAGACGTAATTT 540
QY      181 PheLeuArgGlyIleAspValValSerProAlaAsnAlaAspThrAspValPheIleAsn 200
Db      541 TTCCGCGCGGATAGACGTTGTTCTCTGCAATGCGCAATACAGATGTTTATTTAAC 600
QY      201 IleAspValPheGlyThrIleArgAsnArgThrGluMetHisLeuTyrAsnAlaGluThr 220
Db      601 ATCGACGATATTCGGAAGCATATCGCAACGAAACCCGAAATGCAATCGCCGAAACA 660
QY      221 LeuYsAlaGlnThrIleYsLeuGlyIleThrPheAlaValAspArgThrAsnIleYsLeu 240
Db      661 CTGAAGGCCCAAACTGGAATATTTCCAGTAGACAGAACCAATMAAAATTTGCTC 720
QY      241 IleYsProYsThrAsnAlaPheGluAlaIleTyrIleYsGluAsnTyrAlaLeuThrMet 260
Db      721 ATCAAAACCAAAACCAATGCGTTGAGCTGCTATTAAGAAATTTACGCAATTTGGATG 780
QY      261 GlyProTyrIleYsValSerIleGlyIleYsProThrGlnGlyLeuMetValAspPheSer 280
Db      781 GGGCGGCTAATAAGTAGCAAAAGGAATCAACCGACGAGAGGATGATGCTGATTTCTCC 840
QY      281 AspIleArg-ProTyrGlyIleAsnHisThrGlyAsnSerAlaProSerValGluAlaAspAs 300
Db      841 GATATCCA-ACCATACGCGCAATCATACGCTAATCCGCCCATCCGTAAGGCGCTGAATA 899
QY      300 nSerHisGlnGlyIleYsGlyTyrSerAspGluAlaValArgGlnHisArgGlnGlyIlePr 320
Db      900 CAGTCATAGGGGGTATGATTCACGCGATGAAGCACTGCGCAACATTAACAAGGGCAACC 959
QY      320 o 320
Db      960 T 960
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RESULT 4
AAZ54614
ID AAZ54614 standard; DNA; 963 BP.

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XX      XX      AAZ54614;
AC      XX      15-SEP-2003 (revised)
XX      DT      21-MAR-2000 (first entry)
XX      DT      21-MAR-2000 (first entry)
XX      DE      Neisseria gonorrhoeae ORF 406 partial DNA sequence SEQ ID NO:3111.
XX      KW      Neisseria meningitidis; Neisseria gonorrhoeae; antigen; vaccine;
KW      antigenic; diagnosis; immunogenic; infection; meningitis; septicaemia;
XX      KW      antibacterial; gene therapy; ds.
XX      OS      Neisseria gonorrhoeae.
XX      PN      MO9957280-A2.
XX      PD      11-NOV-1999.
XX      PF      30-APR-1999; 99WO-US009346.
XX      PR      01-MAY-1998; 98US-0083758P.
PR      31-JUN-1998; 98US-0094869P.
PR      02-SEP-1998; 98US-0088994P.
PR      02-SEP-1998; 98US-009062P.
PR      09-OCT-1998; 98US-0103749P.
PR      09-OCT-1998; 98US-0103794P.
PR      09-OCT-1998; 98US-0103796P.
PR      25-FEB-1999; 99US-0121528P.
XX      PA      (CHIR ) CHIRON CORP.
PA      (GENO-) INST GENOMIC RES.
XX      PI      Fraser C, Galeotti C, Grandi G, Hickey E, Masiagnani V, Mora M,
PI      Peteren J, Piazza M, Rappuoli R, Ratti G, Scalato E, Scarselli M,
PI      Teterlin H, Venter JC;
XX      WPI; 2000-062150/05.
DR      P-PSDB; AAY75812.
XX      PT      Novel Neisserial polypeptides predicted to be useful antigens for
PT      vaccines and diagnostics.
XX      PS      Example 1; Page 109; 1453pp; English.
XX      CC      AAZ53015 to AAZ54536, AAZ54577 to AAZ54615, and AAY74253 to AAY75941
CC      represent novel Neisseria meningitis and N. gonorrhoeae polynucleotides
CC      and polypeptides. AAZ54537 to AAZ54576 and AAZ54616 to AAZ5473 represent
CC      PCR primers used in the exemplification of the present invention. The
CC      polypeptides, the polynucleotides, antibodies and compositions of the
CC      invention can be used as vaccines, as diagnostic reagents, and as
CC      immunogenic compositions. The polypeptides can be used in the manufacture
CC      of medicaments for treating or preventing infection due to Neisserial
CC      bacteria (e.g. meningitis and septicaemia), to detect the presence of
CC      Neisseria bacteria, or to raise antibodies. They may also be used to
CC      screen for agonists or antagonists, which may themselves have use as
CC      antibacterial agents. The polynucleotides of the invention may also be
CC      used in gene therapy protocols. (updated on 15-SEP-2003 to standardise OS
CC      field)
XX      SQ      Sequence 963 BP; 276 A; 241 C; 226 G; 220 T; 0 U; 0 Other;
```

Alignment Scores:

Pred. No.:	1,21e-279	Length:	963
Score:	282.00	Matches:	319
Percent Similarity:	99.38%	Conservative:	0
Best Local Similarity:	99.38%	Mismatches:	1
Query Match:	88.12%	Indels:	2
DB:	3	Gaps:	0

US-10-617-835-4 (1-320) x AAZ54614 (1-963)

QY 1 MetArgAlaArgLeuLeuIleProIleLeuPheSerValPheIleLeuSerAlaCysGly 20
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Db      1 ATGGGGGACGGCTGCTGATACCTATCTTTTTCAGTTTATTTTATCCGGCTGGCGG 60
Qy      21 ThrLeuThrGlyIleProSerHisglYglYlybAspPheAlaValIcIuIngluIeu 40
Db      61 ACACGACACGAGTATTCATCGCATGCGGAGGCAACGCTTCGCGGTCCAAACAAGACTT 120
Qy      41 ValAlaIaSerAlaArgAlaAlaValLybAspMetAspLeuAlaIleuHisglYArg 60
Db      121 GTGGCCGCTTCGCGAGAGCTCCGTTTAAAGACATGGATTTCAGGCATTACCGACGA 180
Qy      61 LybValAlaLeuTyrlIeAlaTherMetGlyAspGInglySerGlySerLeuThrGly 80
Db      181 AAAGTTGATTTTACATTGCACTATGGCGACCAAGGTTTCAAGGAGTTTGACAGGGGCT 240
Qy      81 ArgIYSerIleAspAlaLeuIleArgglYglYtyrlIeAsnSerProAlaValArgThr 100
Db      241 CGCTACTCCATTTGATGACACTGATTCGCGCGGAGTATCAATCAAGCCCTGCGCACCC 300
Qy      101 AspIYrThrIYrProArgIYrGlyuThrAlaIuThrThrSerGlyGlyLeuThrGly 120
Db      301 GATTACACCTATCCCGGTACCAAAACACCGCTGAAACAACATCAAGCGGTTTGACGGGT 360
Qy      121 LeuThrThrSerLeuSerThrLeuAsnAlaProAlaLeuSerArgThrGInSerAspGly 140
Db      361 TTAAACCACTTCTTTATCTACACTTAATGCCCTGCACTCTCGCGACCCCAATCAGACGGT 420
Qy      141 SerGlySerArgSerSerleuGlyLeuAsnIleGlyGlyMetGlyAspIYrArgAnglu 160
Db      421 AGCGGAGAGAGAGAGAGTCTGGCTTAAATATTGGCGGAGTATGGAATGTA 480
Qy      161 ThrLeuThrThrAsnProArgAspThrAlaPheLeuSerHisLeuValGInThrValPhe 180
Db      481 ACCTTGACGACCAACCCCGCGACACAGCTCTTTCTTCCACTGGTGACGCCGTAATT 540
Qy      181 PheLeuArgGlyIleAspValValSerProAlaAsnAlaAspThrAspValPheIleAsn 200
Db      541 TTCCTGCGCGGACATAGACGTTCTTCTCTGCGCAATGCCGATACAGATGTTTATTAC 600
Qy      201 IleAspValPheGlyThrIleArgAsnArgThrGlyMetHisLeuIYrAsnAlaGluThr 220
Db      601 ATCGACGATTCGGAACGATACGCAACAGAACCGAAATCACTATACAAATCCGAAACA 660
Qy      221 LeuIYrAlaGInThrIYrleuGluIYrPheAlaValAspArgThrAsnIYrleuIeu 240
Db      661 CTGAAGACCCCAACAAACTGGAATATTTGCGAGTAGACAGAACCAATTAATAAATTGCTC 720
Qy      241 IleIYrProIYrThrAsnAlaPheGluAlaIaIaIYrGlyAsnIYrAlaLeuTrpMet 260
Db      721 ATCAAAACCAAAACCAATGCCGTTTGAAGCTGCTTAAAGAAATTAACCATTTGGAGATG 780
Qy      261 GlyProIYrIYrValSerIYrGlyIleIYrProThrGluGlyLeuMetValAspPheSer 280
Db      781 GGGCGGATTAAGTAAGCAAAAGAAATCAAAACGACGAGGAGTATGATGATTTCTCC 840
Qy      281 AspIleAsnArg-ProIYrGlyIYrAsnHisThrGlyIYrAsnSerAlaProSerValGluAlaAspAs 300
Db      841 GATATATCCA-ACCATACGGGCAATCATACGGGTAATCTCCGCAATCCGTAAGAGGCTGATDA 899
Qy      300 nSerHisglIuGlyTYrGlyTYrSerAspGluAlaValArgGInHisArgGInglyIuIe 320
Db      900 CAGTCATGAGGGGTTATGATATACAGATGACAGTACGACCAACATATAGCAAGGGCAACC 959
Qy      320 o 320
Db      960 T 960

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RESULT 5
 AA253688
 ID AA253688 standard; DNA; 963 BP.
 AC AA253688;
 XX
 DT 15-SEP-2003 (revised)

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DT      21-MAR-2000 (first entry)
XX
DE      Neisseria gonorrhoeae ORF 406 partial DNA sequence SEQ ID NO:1325.
XX
KW      Neisseria meningitidis; Neisseria gonorrhoeae; antigen; vaccine;
KW      antigenic; diagnosis; immunogenic; infection; meningitis; septicemia;
KW      antibacterial; gene therapy; ds.
XX
OS      Neisseria gonorrhoeae.
XX
PN      WO9597280-A2.
XX
PD      11-NOV-1999.
XX
PF      30-APR-1999; 99WO-US009346.
XX
PR      01-MAY-1998; 98US-0083758P.
PR      31-JUL-1998; 98US-0094869P.
PR      02-SEP-1998; 98US-0098994P.
PR      02-SEP-1998; 98US-0099063P.
PR      09-OCT-1998; 98US-0103743P.
PR      09-OCT-1998; 98US-0103794P.
PR      09-OCT-1998; 98US-0103796P.
PR      25-FEB-1999; 99US-0121528P.
XX
PA      (CHIR) CHIRON CORP.
PA      (GENO-) INST GENOMIC RES.
XX
PI      Frazer C, Galeotti C, Grandi G, Hickey E, Masignani V, Mora M,
PI      Petersen J, Pizzo M, Rapunoli R, Ratti G, Scalato E, Scarselli M,
PI      Tettelin H, Venter JC;
XX
DR      WPI: 2000-062150/05.
XX
P-PSDB: AA74926.
XX
PT      Novel Neisserial polypeptides predicted to be useful antigens for
PT      vaccines and diagnostics.
XX
PS      Claim 7; Page 728; 1453pp; English.
XX
CC      AA253015 to AA254536, AA254577 to AA254615, and AA74253 to AA75941
CC      represent novel Neisseria meningitidis and N. gonorrhoeae polynucleotides
CC      and polypeptides; AA254537 to AA254576 and AA254616 to AA255473 represent
CC      PCR primers used in the exemplification of the present invention. The
CC      polypeptides, the polynucleotides, antibodies and compositions of the
CC      invention can be used as vaccines, as diagnostic reagents, and as
CC      immunogenic compositions. The polypeptides can be used in the manufacture
CC      of medicaments for treating or preventing infection due to Neisserial
CC      bacteria (e.g. meningitis and septicemia), to detect the presence of
CC      Neisseria bacteria, or to raise antibodies. They may also be used to
CC      screen for agonists or antagonists, which may themselves have use as
CC      antibacterial agents. The polynucleotides of the invention may also be
CC      used in gene therapy protocols. (Updated on 15-SEP-2003 to standardise OS
CC      field)
XX
SQ      Sequence 963 BP; 276 A; 241 C; 226 G; 220 T; 0 U; 0 Other.
XX
Alignment Scores:
Pred. No.: 1,21e-279 Length: 963
Score: 282.00 Matches: 319
Percent Similarity: 99.38% Conservative: 0
Best Local Similarity: 99.38% Mismatches: 1
Query Match: 88.12% Indels: 2
DB: Gaps: 0
US-10-617-835-4 (1-320) x AA253688 (1-963)
Qy      1 MetArgAlaArgGluLeuIleProIleuPheSerValPheIleLeuSerAlaCysGly 20
Db      1 ATGGGGGACGGCTGCTGATACCTATCTTTTTCAGTTTATTTTATCCGGCTGGCGG 60
Qy      21 ThrLeuThrGlyIleProSerHisglYglYlybAspPheAlaValIcIuIngluIeu 40

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Dh 61 ACACGACAGGATATTCATCCATGCGAGGCAAAACGCTTCGCGGTGCAACAAACCTT 120
Qy 41 ValAlaAlaSerAlaArgAlaAlaValAlaSerMetAspLeuGlnAlaLeuHisGlyArg 60
Dh 121 GTGGCGGCTTGTCCAGAGCTGCGCTTAAAGACATGATTTACAGGCAATACACGAGAGA 180
Qy 61 LysValAlaLeuGlyTyrLeuAlaThrMetGlyAspGlnGlySerGlySerLeuThrGly 80
Dh 181 AAAGTTGATTTGATCATTCGCAACTATGGGCGCACAGGTTTCAAGGATTTGACAGGGGCT 240
Qy 81 ArgTyrSerTyrLeuAspAlaLeuIleArgGlyGlyTyrIleAsnSerProAlaValArgThr 100
Dh 241 CGCTACTCCATTCATGATGACATGATTCGCGCGAATACATTAACAGCCCTGCGCTCGCAC 300
Qy 101 AspTyrThrTyrProArgTyrGlyTyrThrAlaGlnTyrThrSerGlyGlyLeuThrGly 120
Dh 301 GATTACACTTATCCGCGTTACGAAACACCGCTGAAACACATCAGGCGGTTTACGGGCT 360
Qy 121 LeuThrThrSerLeuSerThrLeuAsnAlaProAlaLeuSerArgThrGlnSerAspGly 140
Dh 361 TTAAACACTTCTTATATCTACACTTAATGCCCTGACATCTGCGCACCCCAATCAGACGGT 420
Qy 141 SerGlySerArgSerSerLeuGlyLeuAsnIleGlyGlyMetGlyAspTyrArgAsnGly 160
Dh 421 AGCGAAGTAGACAGACTCTGGCTTAAATATGGCGGATGGGGATTCGAAATGAA 480
Qy 161 ThrLeuThrThrAsnProArgAspThrAlaPheLeuSerHisLeuValGlnThrValPhe 180
Dh 481 ACCTTGACAGCAACCCGCGGACACTGCCCTTTCTTTCCACTGGTGCAGACCGTATTT 540
Qy 181 PheLeuArgGlyIleAspValValSerProAlaAsnAlaAspThrAspValPheIleAsn 200
Dh 541 TTCCTGGCGGCAATAGACGTTGTTCTCTGCAATGCCATACAGATGTTATTTATTAAC 600
Qy 201 IleAspValPheGlyThrIleArgAsnArgThrGlyMetHisLeuTyrAsnAlaGlnThr 220
Dh 601 ATTCACGATTCGGAACCATACGCAACGAAACCGAAATGACCTATTAACAATGCCGAAACA 660
Qy 221 LeuTyrAlaGlnTyrLeuGlyTyrPheAlaValAspArgThrAsnIleLeuLeu 240
Dh 661 CTGAAAGCCCAACAACTGGAATATTTCCGACATGACAGAACCAATMAAAATTTGCTC 720
Qy 241 IleLysProLysThrAsnAlaPheGlnAlaAlaTyrIleGlyAsnTyrAlaLeuTyrMet 260
Dh 721 ATCAAAACCAAAACCAATGCGTTTGAAGCTCTCTATAAGAAATTTACGCAATTCGATG 780
Qy 261 GlyProTyrLysValSerLeuGlyIleLysProThrGlnGlyLeuMetValAspPheSer 280
Dh 781 GGGCCGATTAAGTAAGCAAGAAATCAACCCGACGGAAGGATTTGATGCTGATTTCTCC 840
Qy 281 AspIleArg-ProTyrGlyAsnHisThrGlyAsnSerAlaProSerValGlnAlaAspAs 300
Dh 841 GATATCCA-ACCATACGGCAATCATACGGGTAATCTCCGCCCATCCGTAAGGCTGATA 899
Qy 300 nSerHisGlnGlyTyrGlyTyrSerAspGlnAlaValArgGlnHisArgGlnGlyGlnPr 320
Dh 900 CAGTCATGAGGGGATGATGATACAGCATGAAGCAGTGCAGCAACATGACAAAGGCAACC 959
Qy 320 o 320
Dh 960 T 960

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RESULT 6
AAA81297
ID AAA81297 standard; DNA; 963 BP.

AC AAA81297;
XX 15-SEP-2003 (revised)
DT 04-DEC-2000 (first entry)
XX

DE N. gonorrhoeae partial DNA sequence g406.seq SEQ ID NO:1036.
XX

KW Neisseria meningitidis; Neisseria gonorrhoeae; genome; immunogenic;
KW antigen; vaccine; diagnosis; infection; antibacterial; identification;
KW Meningococcus B; MenB; ds.
OS Neisseria gonorrhoeae.
XX
XX WO200022430-A2.
XX
XX 20-APR-2000.
XX
XX
XX 08-OCT-1999; 99WO-US023573.
XX
XX 09-OCT-1998; 98US-0103794P.
XX 30-APR-1999; 99US-0132068P.
XX
XX (CHIR) CHIRON CORP.
XX
XX Frazer CM, Hickey E, Peterson J, Tetteelin H, Venter JC;
PI Maignani V, Galeotti C, Mora M, Ratti G, Scarselli M, Scarlato V;
PI Rappuoli R, Piza M;
XX
XX WPI: 2000-318079/27.
DR P-PSDB; AAB25657.
DR
XX
XX Isolated nucleotide sequences of Neisseria meningitidis which can be used
PT in the diagnosis and treatment of N. meningitidis infection and other
PT Neisseria infections, for example, N.gonorrhoea.
XX
XX Claim 9; Page 108; 1760pp; English.
XX
XX The present invention describes methods of obtaining immunogenic proteins
CC from Neisseria genomic sequences. AAA81453 to AAA82414 represent
CC specifically claimed Neisseria meningitidis genomic DNA sequences;
CC AAA81260 to AAA81303 and AAB25620 to AAB25663 represent Neisseria DNA
CC sequences and their corresponding proteins; AAA81254 to AAA81259 and
CC AAA81304 to AAA81321 represent PCR primers used in the isolation of
CC Neisseria meningitidis DNA sequences; and AAA81322 to AAA81452 represent
CC Neisseria meningitidis MenB polynucleotide ORF sequences, which are all
CC used in the exemplification of the present invention. The nucleic acid
CC sequences, protein sequences, and antibodies against them, can be used in
CC the manufacture of a composition. The composition can be used as a
CC medicament (or in the manufacture of a medicament) for treating,
CC preventing or diagnosing infection due to Neisseria bacteria. For
CC example, some of the identified proteins could be components of vaccines
CC against Meningococcus B; against all serotypes; and/or against all
CC pathogenic Neisseriae. Identification of sequences from the bacterium
CC will also facilitate production of biological probes, particularly
CC organism-specific probes. Attempts to make efficacious Meningococcus B
CC vaccines have failed mainly due to antigen tolerance. Multivalent
CC antigens have also been tried but none have successfully overcome
CC antigenic variability. The provision of further, complete sequences may
CC provide an opportunity to identify secreted or surface exposed proteins
CC that may be presumed targets for the immune system and which are not
CC antigenically variable or at least more conserved than other more
CC variable regions. (Updated on 15-SEP-2003 to standardise OS field)
XX
SQ Sequence 963 BP; 276 A; 241 C; 226 G; 220 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 1 21e-279 Length: 963
Score: 282.00 Matches: 319
Percent Similarity: 99.38% Conservative: 0
Best Local Similarity: 99.38% Mismatches: 1
Query Match: 88.12% Indels: 2
DB: 3 Gaps: 0

US-10-617-835-4 (1-320) x AAA81297 (1-963)

Qy 1 MechArgAlaArgLeuLeuIlePheIleLeuPheSerValPheIleLeuSerAlaCysGly 20
Dh 1 ATGGCGGACAGCGGCTGATACCATCTTTTTCACATTTTATTTATCTACGCTCGGGG 60
Qy 21 ThrLeuThrGlyIleProSerHisGlyGlyGlyLysArgPheAlaValGlnGlnGlnLeu 40

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Db      61 ACACGACAGCGTATTCATCGATGCGAGCGCAACCGTTCCGCTCGACACAAAGACTT 120
Oy      41 ValAlaAlaSerAlaArgAlaAlaValAlaLysAspMetAspLeuGlnAlaLeuHisGlyArg 60
Db      121 GTGGCCGCTTGTGCGAGAGCTCCGTTAAAGACATGATTTACAGGCAATTAACCGGACGA 180
Oy      61 LysValAlaLeuTyrIleAlaIleMetGlyAspGlnGlySerGlySerLeuThrGlyGly 80
Db      181 AAAGTTGATGTGATGCAATGCAATGAGCGGACCAAGGTTGCGGAGTTTGACAGGGGGT 240
Oy      81 ArgTyrSerIleAspAlaLeuIleArgGlyGlyTyrIleAspSerProAlaValAlaArgThr 100
Db      241 CGCTACTCTCATTTGATGCACTGATTTGCGCGCGAATCACTAAACAGCCCTCGCTCCGACCC 300
Oy      101 AspTyrThrTyrProArgTyrGlyIleThrAlaGlnThrThrSerGlyGlyLeuThrGly 120
Db      301 GATTACACCTATCCCGCTTACGAAACCAACCGCTGAACCAATCAAGCGGCTTGAAGGGGT 360
Oy      121 LeuThrThrSerLeuSerThrLeuAsnAlaProAlaLeuSerArgThrGlnSerAspGly 140
Db      361 TTAAACACCTTTCTTTATCTAACACTTAATGCCCCGCACTCTCGGACCCCAATCAACACGCT 420
Oy      141 SerGlySerArgSerSerLeuGlyLeuAsnIleGlyGlyMetGlyAspTyrArgAsnGly 160
Db      421 AGCGGAAGTAGAGAGAGCTGCGCTTAATATTGGCGGAGTGGGGAATTAATGAAATGAA 480
Oy      161 ThrLeuThrThrAsnProArgAspThrAlaPheLeuSerHisLeuValGlnThrValPhe 180
Db      481 ACCTTGACGACCAACCCCGCGGACACCTGCTTTCTTCCCACTGCTGCGACGCTATATT 540
Oy      181 PheLeuAlaGlyIleAspValValSerProAlaAsnAlaAspThrAspValPheIleAsn 200
Db      541 TTCCTGCGCGGATAGACGTTGTTCTCTCGCAATGCGATACAGATGTTTATTTAC 600
Oy      201 IleAspValPheGlyThrIleArgAsnArgThrGlnMetHisLeuTyrAsnAlaGlnThr 220
Db      601 ATCGACGATTTGCGAACATACGCAACGAAACCGAAATGCACTTATCAATGCCAACA 660
Oy      221 LeuLysAlaGlnThrLysLeuGlyIleThrPheAlaValAspArgThrAsnLysLeuLeu 240
Db      661 CTGAAAGCCCAACAACTGGAAATATTTCGACATAGACAGAACCAATTAATAAATTTGCTC 720
Oy      241 IleLysProLysThrAsnAlaPheGlnAlaAlaTyrLysGluAsnTyrAlaLeuTyrMet 260
Db      721 ATCAAAACCAAAACCAATGCGTTGAACTGCTTAAAGAAATTTAAGCATTTGAGATG 780
Oy      261 GlyProTyrLysValSerLysGlyIleLysProThrGlnGlyLeuMetValAspPheSer 280
Db      781 GGGCGGTTAAAGTAAAGCAAGAAAGATCAAAACGACGAGAAAGATGATGCTGATTTCTCC 840
Oy      281 AspIleArg-ProTyrGlyAsnHisIleThrGlyAsnSerAlaProSerValGlnAlaAspAs 300
Db      841 GATATCCA-ACCATATCGGCATATCATACGGGTAACTCCGCCCATCGTATGAGAGCGTATA 899
Oy      300 nSerHisGlnGlyTyrGlyTyrSerAspGlnAlaAlaArgGlnHisArgGlnGlyGlnPr 320
Db      900 CAGTCATGAGGGGTATGATGATACAGCATGAAGCAATGCGAACATTAACAAGGCGCAACC 959
Oy      320 o 320
Db      960 T 960

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RESULT 7
AAAF21582
ID AAF21582 standard; DNA; 963 BP.
XX
AC AAF21582;
XX
DT 15-SEP-2003 (revised)
DT 13-MAR-2001 (first entry)
XX
N. gonorrhoeae partial DNA sequence g406.seq SEQ ID NO:76.

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XX      XX Neisseria meningitidis; Neisseria gonorrhoeae; immunogenic; vaccine;  
KM      KM diagnosis; antigen; detection; infection; gene therapy; antibacterial;  
KW      KW de.  
XX      XX  
OS      OS Neisseria gonorrhoeae.  
XX      XX  
PN      PN WO200066791-A1.  
XX      XX  
PD      PD 09-NOV-2000.  
XX      XX  
PF      PF 08-MAR-2000; 2000WO-US005928.  
XX      XX  
PR      PR 30-APR-1999; 99US-0132068P.  
PR      PR 08-OCT-1999; 99WO-US023573.  
PR      PR 28-FEB-2000; 2000GB-00004695.  
XX      XX  
PA      PA (CHIR) CHIRON CORP.  
PA      PA (GENO-) INST GENOMIC RES.  
XX      XX  
PI      PI Pizza M, Hickey E, Peterson J, Tetteijn H, Venter JC,  
PI      PI Maignani V, Galeotti C, Mora M, Ratti G, Scarselli M, Scarlato V;  
PI      PI Rapunoli R, Frazer CM, Grandi G;  
XX      XX  
DR      DR MPI, 2000-647603/62.  
DR      DR P-PSDB; AAB58587.  
XX      XX  
PT      PT Neisseria meningitidis B full length genome sequence and open reading  
PT      PT frames are used to detect, treat and prevent Neisserial infections.  
XX      XX  
PS      PS Example 1; Page 109; 692pp; English.  
XX      XX  
CC      CC The present invention describes the full length genome of Neisseria  
CC      CC meningitidis B (NMB). The sequences in AAF21544 and AAF21607 to AAF21613  
CC      CC represent fragments of the NMB genomic sequence, as the sequence which  
CC      CC long to go in a record on its own it was split into 8 sequences which  
CC      CC overlap each other at the beginning and end of each sequence by 4980 bp  
CC      CC (i.e. the last 4980 bp of AAF21544 is repeated at the beginning of  
CC      CC AAF21607, the last 4980 bp of AAF21607 are repeated at the beginning of  
CC      CC AAF21608, and so on). AAF21545 to AAF21588 encode the Neisseria proteins  
CC      CC given in AAB58550 to AAB58593, and AAF21589 to AAF21606 represent PCR  
CC      CC primers which are used in the exemplification of the present invention.  
CC      CC The NMB genome and fragments from it have antibacterial activity, and can  
CC      CC be used in vaccines and gene therapy. Neisseria nucleic acids, proteins  
CC      CC and/or antibodies which bind to the proteins can be used in compositions  
CC      CC for treating or preventing infection due to Neisserial bacteria or as a  
CC      CC diagnostic reagent for detecting the presence of Neisserial bacteria or  
CC      CC of antibodies raised to Neisserial bacteria. Computers, computer memory,  
CC      CC computer storage medium or computer databases can be used in a search to  
CC      CC identify open reading frames (ORFs) or coding sequences within the NMB  
CC      CC genome. The DNA sequences provide further opportunities to find antigenic  
CC      CC or immunogenic proteins which are more effective in vaccines than the  
CC      CC outer membrane proteins currently used. (Updated on 15-SEP-2003 to  
CC      CC standardise OS field)  
XX      XX  
SQ      SQ Sequence 963 BP; 276 A; 241 C; 226 G; 220 T; 0 U; 0 Other;  
XX      XX  
Alignment Scores:  
Pred. No.: 1,21e-279 Length: 963  
Score: 282.00 Matches: 319  
Percent Similarity: 99.38% Mismatches: 0  
Best Local Similarity: 99.38% Indels: 2  
Query Match: 88.12% Gaps: 0  
DB: 3  
US-10-617-835-4 (1-320) x AAF21582 (1-963)  
Oy      Oy 1 MetArgAlaArgLeuLeuIleProIleLeuPheSerValPheIleLeuSerAlaCysGly 20  
Db      Db 1 ATGCGGCGACGCGCTGATACCTATTTCTTTTTCAGTTTATTTATTCGCGCGCGG 60  
Oy      Oy 21 ThrLeuThrGlyIleProSerHisGlyGlyLysArgPheAlaValGlnGlnLeu 40

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Db      61  ACACGACAGGATTCATCGCATGCGAGGCAAAACGCTTCGCGGTGCAACAAGAACTT 120
Qy      41  ValAlaAlaSerAlaArgAlaAlaValLysAspMetAspLeuGlnAlaLeuHisGlyArg 60
Db      121  GTGGCCGCTTCCTGCGAGAGCTGCGGTAAAGACATGATTTACAGGCACTTACACGACGA 180
Qy      61  LysValAlaLeuTyrIleAlaThrMetGlyAspGlnGlySerGlySerLeuThrGlyGly 80
Db      181  AAAGTTGATTTGATTCATTCGCAACTATGCGGCAAGATTACAGGCACTTACAGGAGG 240
Qy      81  ArgTyrSerIleAspAlaLeuIleArgGlyGlyTyrIleAsnSerProAlaValArgThr 100
Db      241  CGCTACTCCATTGATGACCTGATTCGCGGCAATTCATAAACAGCCCTGCGGCACCC 300
Qy      101  AspTyrThrTyrProArgTyrGlyThrThrAlaGlyuThrThrSerGlyGlyLeuThrGly 120
Db      301  GATTACACCTATCCGCGTTACGAACCAACCGGTGAACACATCCAGGCGGTTTGCGGGT 360
Qy      121  LeuThrThrSerLeuSerThrLeuAsnAlaProAlaLeuSerArgThrGlnSerAspGly 140
Db      361  TTAAACCACTTCTTATATCTACACTTATATGCCCTGCACTCGCGCACCCCAATCAGAGCGT 420
Qy      141  SerGlySerArgSerSerLeuGlyLeuAsnIleGlyGlyMetGlyAspTyrArgAsnGlu 160
Db      421  AGCGGAAGTAGACAGACAGTCTGCGCTTAAATATGCGGGAATGCGGGGATTCAGAAATGAA 480
Qy      161  ThrLeuThrThrAsnProArgAspThrAlaPheLeuSerHisIleLeuValGlnThrValPhe 180
Db      481  ACCTTGACGACCAACCCGCGGACACTGCTCTTCTTCCACTGGTGACAGCGTATTT 540
Qy      181  PheLeuArgGlyIleAspValValSerProAlaAsnAlaAspThrAspValPheIleAsn 200
Db      541  TTCTCGGCGCGCATAGACGTTGTTCTCTCGCAATCGCATACAGATGCTTTATTATAC 600
Qy      201  IleAspValPheGlyThrIleArgAsnArgThrGlyMetHisIleuTyrAsnAlaGlyThr 220
Db      601  ATCCACGATTCGGAACGATACGCAACAGAACCCGAAATGACCTATACAAATGCCGAAACA 660
Qy      221  LeuTyrAlaGlnThrTyrLysLeuGlyuTyrPheAlaValAspArgThrAsnLysLeuLeu 240
Db      661  CTGAAAGCCCAACAAACCTGGAATATTTCCGAGTAGACAGAACCAATTAATAATTGCTC 720
Qy      241  IleLysProLysThrAsnAlaPheGlyAlaAlaIleTyrLysGlyAsnTyrAlaLeuTyrMet 260
Db      721  ATCAAAACCAAAACCAATGCGTTGAACTGCTCATTAAGAAATTACGCACTTGCGATG 780
Qy      261  GlyProTyrLysValSerLysGlyIleLysProThrGlyGlyLeuMetValAspPheSer 280
Db      781  GGGCCGATTAAGTAAGCAAGCAATCAACCGACGGAAGATTGATGCTGATTTCTCC 840
Qy      281  AspIleArg-ProTyrGlyAsnHisIleThrGlyAsnSerAlaProSerValGlyAlaAspAs 300
Db      841  GATATCCA-ACCATACGCGCAATCATACGGGTAACTCCGCCCATCCGTAAGGCTGATTA 899
Qy      300  nSerHisGlyGlyTyrGlyTyrSerAspGlyAlaValArgGlnHisArgGlnGlyGlnPr 320
Db      900  CAGTCATGAGGGGATGATGATACAGCATGAGAGCAGTGGCAACATAGACAAGGCAACC 959
Qy      320  C 320
Db      960  T 960

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RESULT 8
ABZ40799
ID ABZ40799 standard; DNA; 789 BP.
XX ABZ40799;

DT 07-MAR-2003 (first entry)

DE N. gonorrhoeae nucleotide sequence SFG ID 6187.

XX Antibacterial; infection; vaccine; gene therapy; gene; ds.

```

XX      OS  Neisseria gonorrhoeae.
XX      EN  W0200279243-A2.
XX      PD  10-OCT-2002.
XX      PF  12-FEB-2002; 2002MO-IB002069.
XX      PR  12-FEB-2001; 2001GB-00003424.
XX      PA  (CHIR-) CHIRON SPA.
XX      PI  Fontana MR, Pizsa M, Masiagnani V, Monaci E;
XX      DR  WPI: 2003-058415/05.
XX      PT  P-PSDB; ABP79829.
XX      PS  New protein from Neisseria gonorrhoeae, useful for the manufacture of a
XX      PT  medicament for treating or preventing N. gonorrhoeae infection.
XX      PS  Disclosure; Page 639; 815pp; English.
XX      CC  The present invention relates to proteins from Neisseria gonorrhoeae.
XX      CC  Also disclosed are the nucleic acid molecules encoding the proteins and
XX      CC  antibodies that specifically bind to the proteins. The composition
XX      CC  comprising the protein, nucleic acid or antibody is useful for the
XX      CC  manufacture of a medicament for treating or preventing N. gonorrhoeae
XX      CC  infection, this may be in the form of a vaccine or gene therapy.
XX      CC  Sequences given in records ABZ37706-ABZ42016 represent nucleic acid
XX      CC  molecules of the invention
XX      SO  Sequence 789 BP; 217 A; 203 C; 181 G; 188 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 4.91e-254 Length: 789
Score: 257.00 Matches: 257
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatch: 0
Query Match: 80.31% Indels: 0
DB: Gaps: 0

US-10-617-835-4 (1-320) x ABZ40799 (1-789)
Qy      1  MeArGAlaArgLeuLeuIleProIleLeuPheSerValPheIleLeuSerAlaCyGly 20
Db      1  ATGGGGGACAGCGCTGCGATACCATTTCTTTTCACTTTTATATCGGCTGGGG 60
Qy      21  ThrLeuThrGlyIleProSerHisGlyGlyLysArgPheAlaValGlnGlnLeu 40
Db      61  ACACGACAGGATTCATCGCATGCGGAGGCAAAACGCTTCGCGGTGCAACAAGAACTT 120
Qy      41  ValAlaAlaSerAlaArgAlaAlaValLysAspMetAspLeuGlnAlaLeuHisGlyArg 60
Db      121  GTGGCCGCTTCCTGCGAGAGCTGCGGTAAAGACATGATTTACAGGCACTTACAGGACGA 180
Qy      61  LysValAlaLeuTyrIleAlaThrMetGlyAspGlnGlySerGlySerLeuThrGlyGly 80
Db      181  AAAGTTGATTTGATTCATTCGCAACTATGCGGCAAGATTACAGGCACTTACAGGAGG 240
Qy      81  ArgTyrSerIleAspAlaLeuIleArgGlyGlyTyrIleAsnSerProAlaValArgThr 100
Db      241  CGCTACTCCATTGATGACCTGATTCGCGGCAATTCATAAACAGCCCTGCGGCACCC 300
Qy      101  AspTyrThrTyrProArgTyrGlyuThrThrAlaGlyuThrThrSerGlyGlyLeuThrGly 120
Db      301  GATTACACCTATCCGCGTTACGAACCAACCGGTGAACACATCCAGGCGGTTGACGGGT 360
Qy      121  LeuThrThrSerLeuSerThrLeuAsnAlaProAlaLeuSerArgThrGlnSerAspGly 140
Db      361  TTAAACCACTTCTTATATCTACACTTATATGCCCTGCACTCGCGCACCCCAATCAGAGCGT 420
Qy      141  SerGlySerArgSerSerLeuGlyLeuAsnIleGlyGlyMetGlyAspTyrArgAsnGlu 160

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Db      421  AGCGAAGTAGAGACGAGTCTGGCTTAATATTGGCGGATGGGATTAATGAAATGA 480
Qy      161  ThrLeuThrThrAsnProArgAspThrAlaPheLeuSerHisLeuValGlnThrValPhe 180
Db      481  ACCCTGACGACCAACCCGCGGACACTGCTTCTTCCCACTGGTGACAGCCGATATT 540
Qy      181  PheLeuArgGlyIleAspValValSerProAlaAsnAlaAspThrAspValPheIleAsn 200
Db      541  TTCCTGCGGCGATAGACGTTGTTCTCTGCGCAATGCGATACAGATGTGTTATTAAAC 600
Qy      201  IleAspValPheGlyThrIleArgAsnArgThrGluMetHisLeuThrAsnAlaGluThr 220
Db      601  ATCGACGATTTTCGGAACGATACGACACACAAACCGAAATGACCTATACATGCCAAACA 660
Qy      221  LeuValAlaGlnThrIleLeuGluThrPheAlaValAspArgThrAsnValLeuLeu 240
Db      661  CTGAAGCCCAACAAACCTGGAATATTTCGCGAGTAGACAGAACCAATAAATAATGCTC 720
Qy      241  IleValProValThrThrAsnAlaPheGluAlaIleValIleValGluAsnValAla 257
Db      721  ATCAAAACCCAAACCAATGCTTTGAAAGCTGCTATTAAGAAATTAATGAGCC 771

RESULT 9
AAZ12006 standard, DNA; 963 BP.
XX      AAZ12006;
XX      08-OCT-1999 (first entry)
XX      Neisseria meningitidis strain B complete ORF15 sequence.
XX      Neisseria meningitidis; Neisseria gonorrhoeae; antigen; vaccine;
XX      treatment; Neisseria infection; meningitis; septicemia; gonorrhea; ss.
XX      OS
XX      Neisseria meningitidis.
XX      PN
XX      W09924578-A2.
XX      20-MAY-1999.
XX      09-OCT-1998; 98W0-1B00165.
XX      06-NOV-1997; 97GB-00023516.
XX      14-NOV-1997; 97GB-00024190.
XX      18-NOV-1997; 97GB-00024386.
XX      27-NOV-1997; 97GB-00025158.
XX      10-DEC-1997; 97GB-00026147.
XX      14-JAN-1998; 98GB-00000759.
XX      01-SEP-1998; 98GB-00019016.
XX      (CHIR-) CHIRON SPA.
XX      PA
XX      Maegmani V, Rappuoli R, Pizza M, Scarlato V, Grandi G;
XX      WPI, 1999-327407/27.
XX      P-PSDB; AAY38538.
XX      Proteins from Neisseria meningitidis and N. gonorrhoeae useful for
XX      diagnosis, treatment and prevention of infection.
XX      Claim 9, Page 98; 524pp; English.
XX      PS
XX      Nucleotide sequences AAZ11972-212358 represent open reading frames (ORFs)
XX      of Neisseria meningitidis and N. gonorrhoeae which encode antigenic
XX      proteins (see AAY38499-Y38944). The antigenic proteins, their fragments,
XX      their nucleic acids and antibodies are used for diagnosis, prevention (as
XX      vaccines) or treatment of Neisseria infections, such as meningitis,
XX      septicemia and gonorrhea. Both organisms are closely related. Fragments
XX      of the nucleic acids are useful as hybridisation probes and antisense
XX      reagents

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SQ      Sequence 963 BP; 284 A; 234 C; 217 G; 228 T; 0 U; 0 Other;
Alignment Scores:
Pred. No.: 1,46e-202
Score: 207.00
Percent Similarity: 99.35%
Best Local Similarity: 99.35%
Query Match: 64.69%
DB: 2 Gaps: 0
US-10-617-835-4 (1-320) x AAZ12006 (1-963)
Qy      3  AlaArgLeuLeuIleProIleLeuPheSerValPheIleLeuSerAlaCysGlyThrLeu 22
Db      7  GCACGCGCTGCTATACCTATCTTTTTCAGTTTATTATTATTCGCCGCTGGGACACTG 66
Qy      23  ThrGlyIleProSerHisGlyGlyValArgPheAlaValGluGlnIleLeuValAla 42
Db      67  ACAGGATTCATCCGATGCGGAGGTAAAGCTTTGGCGTGMACAAAGAACTGTGGCC 126
Qy      43  AlaSerAlaArgAlaAlaValIleAspMetAspLeuGlnAlaLeuHisGlyValGlyVal 62
Db      127  GCTTCTGCCAGAGCTGCGCTTAAAGACATGATTTACAGGCATTTACACGACGAAAGATT 186
Qy      63  AlaLeuThrIleAlaThrMetGlyAspGlnGlySerGlySerLeuThrGlyIleArgTyr 82
Db      187  GCATGTACATTTGCCATATGAGGCGACACAAAGTTTACGACGTTTACAGGGGGGCTTAC 246
Qy      83  SerIleAspAlaLeuIleArgGlyGlyIleAsnSerProAlaValArgThrAspTyr 102
Db      247  TCATTTGATGACACTGATTTGTCGCGAATACATTAACAGCCCTGCGCTGACCATAC 306
Qy      103  ThrTyrProArgTyrGlyIleThrAlaGluThrThrSerGlyGlyLeuThrGlyLeuThr 122
Db      307  ACCATTCACAGTTAGAAACCAACCGCTGAACACATCAGGGGTTGACAGGTTAACCC 366
Qy      123  ThrSerLeuSerThrLeuAsnAlaProAlaLeuSerArgThrGlnSerAspGlySerGly 142
Db      367  ACTTCTTTATCTACACTTATATGCCCCCTGCACTCTCTCGACCCATCAGACGGTAGCGGA 426
Qy      143  SerArg-SerSerLeuGlyLeuAsnIleGlyGlyMetGlyAspTyrArgAsnGluThrIle 162
Db      427  ACTAA-AAGCAGTCTGGGCTTAATATTGGCGGATGGGAGATTACGAAATGAACCTT 485
Qy      162  uThrThrAsnProArgAspThrAlaPheLeuSerHisLeuValGlnThrValPhePheIle 182
Db      486  GACGACTAACCCGCGCGACACTGCTTCTTCCCACTGGTAGACAGCCGATATTTTCTCT 545
Qy      182  uArgGlyIleAspValIleSerProAlaAsnAlaAspThrAspValPheIleAsnIleAs 202
Db      546  GCGCGCATAGACGTTGTTCTCTGCGCAATGCCATACAGATGTGTTATTAAACATGCA 605
Qy      202  PValPheGlyThrIleArgAsnArgThrGluMetHisLeuThrAsnAlaGluThrLeuVal 222
Db      606  CGTATTCGGAACGATACGCAACAGAACCGAAATGACCTATCAATAGCGGAACACTGAA 665
Qy      222  AlaGlnThrIleValLeuGluThrPheAlaValAspArgThrAsnValGlyLeuLeuIleVal 242
Db      666  AGCCCAACCAAAACCTGGAATATTTCGAGTAGACAGAACCAATTAATAATTTCTCATCA 725
Qy      242  AspProValThrAsnAlaPheGluAlaIleValIleValGluAsnValIleValIleVal 262
Db      726  ACCCAAAACCAATGCGTTTGAAGCTGCTTATTAAGAAATTAACGATTTGTGATGGGGCC 785
Qy      262  OTyrIleValSerIleValGlyIleValProThrGlnGlyLeuMetValAspPheSerAspIle 282
Db      786  GTATTAAGTAAGCAAGAAGATTAACACGACGAAAGATTAAGTGCGATTTCTCGATAT 845
Qy      282  eArgProTyrGlyIleAsnHisThrGlyAsnSerIleProSerValGluAlaAspAsnSerHis 302
Db      846  CCGACCATACGGCAATCATACGGGTAACTCCGCCCATCTCGTAAGGCTGATTAACAGTCA 905
Qy      302  eGluGlyTyrGlyTyrSerAspGlu 310

```

Db 906 TGAGGGGTATGATACAGCATGAA 930
|||||
RESULT 10
AAZ53689
ID AAZ53689 standard; DNA; 963 BP.
XX
AC AAZ53689;
XX
DT 21-MAR-2000 (first entry)
XX
DE Neisseria meningitidis ORF 406 partial DNA sequence SEQ ID NO:1327.
XX
KW Neisseria meningitidis; Neisseria gonorrhoeae; antigen; vaccine;
KW antigenic; diagnostic; immunogenic; infection; meningitis; septicemia;
KW antibacterial; gene therapy; ds.
XX
OS Neisseria meningitidis.
XX
PN MO9957280-A2.
XX
XX 11-NOV-1999.
PD
XX 30-APR-1999; 99WO-US009346.
PF
XX 01-MAY-1998; 98US-0083758P.
PR 31-JUL-1998; 98US-0094869P.
PR 02-SEP-1998; 98US-0098994P.
PR 02-SEP-1998; 98US-0099062P.
PR 09-OCT-1998; 98US-0103749P.
PR 09-OCT-1998; 98US-0103749P.
PR 09-OCT-1998; 98US-0103796P.
PR 25-FEB-1999; 99US-0121528P.
XX
PA (CHIR) CHIRON CORP.
PA (GENO-) INST GENOMIC RES.
PI Fraser C, Galeotti C, Grandi G, Hickey E, Masignani V, Mora M;
PI Petersen J, Pizsa M, Rappuoli R, Ratti G, Scalato E, Scarselli M;
PI Terelein H, Venter JC;
PI
DR WPI; 2000-062150/05.
DR P-PSDB; AAY74927.
XX
PT Novel Neisserial polypeptides predicted to be useful antigens for
PT vaccines and diagnostics.
XX
PS Claim 7; Page 728; 1453pp; English.
XX
XX AAZ53015 to AAZ54536, AAZ54577 to AAZ54615, and AAY74253 to AAY75941
CC represent novel Neisseria meningitidis and N. gonorrhoeae polynucleotides
CC and polypeptides. AAZ54537 to AAZ54576 and AAZ54616 to AAZ54773 represent
CC PCR primers used in the exemplification of the present invention. The
CC polypeptides, the polynucleotides, antibodies and compositions of the
CC invention can be used as vaccines, as diagnostic reagents, and as
CC immunogenic compositions. The polypeptides can be used in the manufacture
CC of medicaments for treating or preventing infection due to Neisserial
CC bacteria (e.g. meningitis and septicemia), to detect the presence of
CC Neisseria bacteria, or to raise antibodies. They may also be used to
CC screen for agonists or antagonists, which may themselves have use as
CC antibacterial agents. The polynucleotides of the invention may also be
CC used in gene therapy protocols
XX
SQ Sequence 963 BP; 284 A; 234 C; 217 G; 228 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 1.46e-202 Length: 963
Score: 207.00 Matches: 307
Percent Similarity: 99.35% Conservatve: 0
Best Local Similarity: 99.35% Mismatches: 1
Query Match: 64.69% Indels: 2
DB: 3 Gaps: 0

US-10-617-835-4 (1-320) x AAZ53689 (1-963)
QY 3 AAlarGleuLeuIIleProIIleuPheSerValPheIIleuSerAlaCyGlyThrLeu 22
Db 7 GCACGGCTGCTGATACCTATCTTTTTCAGTTTATTTATCCGCTGGGGCAGCTG 66
QY 23 ThrGlyIleProSerHieGlyGlyYlySarGpheaIaValGluGlnGluLeuValAla 42
Db 67 ACAGGTATTCATCGCATGGCGGAGTAAAGCTTTGGCGTCGAACAAGAACTTGCGC 126
QY 43 AlaserAlaargAlaIaValIyaspMetaspLeuGlnAlaLeuHieGlyArgIyVal 62
Db 127 GCTTCTGCACAGCTGCCGTTAAAGACATGATTTTACAGCATTTACAGGACGAAGACTT 186
QY 63 AlaleuTrIlealathMetGlyAspGlnGlySerGlySerLeuThrGlyIArgThr 82
Db 187 GCATGTGACATGACCATGAGGCGACCAAGGTTGAGGAGTTTGACAGGGGGTGGCTAC 246
QY 83 SerIleaspAlaleuIleargGlyGluThrIleaspSerProAlaValArgThrAspThr 102
Db 247 TCCATGTGATGACGATTCGTGGCGAATACATAAAGCCCTGCGTCCGTACCGATTAC 306
QY 103 ThrTyProArgTyGluThrThrAlaGluThrThrSerGlyIleuThrGlyLeuThr 122
Db 307 ACCTATCCACGTTACGAACACACCGCTGAACAACATCAGCGGTTGACAGTTTAAAC 366
QY 123 ThrSerIleuSerThrIleaspAlaProAlaleuSerArgThrGlnSerAspGlySerGly 142
Db 367 ACTCTTATATTAACCTTAAGCCCTGACATCTCTGACCCATCAGAGGTAGCGGA 426
QY 143 SerArg-SerSerIleuGlyLeuAsnIleGlyIyMeGlyAspTyArgAsnGluThrIle 162
Db 427 AGTAA-AAGCAGCTGGGCTTAATATTTGGGGGATATGAAATGAACCTT 485
QY 162 uThrThrAsnProArgAspThrAlaPheLeuSerHieLeuValGlnThrValPhePheLe 182
Db 486 GACGACATAACCCGGCGCACACCTGCTTCTTCCACCTGGTACAGACCGTATTTTCT 545
QY 182 uArgGlyIleAspValIleSerProAlaAsnAlaAspThrAspValPheIleAsnIleAs 202
Db 546 GCGCGCATACGCTGTGTTCTGCGCAAGCCGATACAGATGTGTTTATTAACATCGA 605
QY 202 PvalPheGlyThrIleArgAsnArgThrGluMetHieLeuTyRsnAlaGluThrLeuTy 222
Db 606 CGTATTTGGAACGATACGCAACAGAACCGAAATGCTACCTATACATGCCGAACATCGAA 665
QY 222 sAlaGlnThrIyLeuGluTyRheaIaValAspArgThrAsnIyIyLeuIleTy 242
Db 666 AGCCCAACCAAACTGGAATATTTCCGACGTAGACAGAACCAATTAATAATTTGCTCATCAA 725
QY 242 sProIyThrAsnAlaPheGluAlaIaTyRlyGluAsnTyRAlaLeuTyRMetGlyPr 262
Db 726 ACCAAACCAATCGTTGAGCTGCTTAAGAAATTAAGAAATTAAGCAATTTGAGAGGGGCC 785
QY 262 oTyRlyValSerIyGlyIleTyProThrGluGlyLeuMetValAspPheSerAspI 282
Db 786 GTATTAAGTAAGCAAGAAATTAACCGACGAAAGATTAATGCTCATTTCTCGATAT 845
QY 282 eArgProTyRglyAsnHieThrGlyAsnSerAlaProSerValGluAlaAspAsnSerHie 302
Db 846 CCGACCATACGCGCATATACGGGTAACTCCGCCCATCGTAAAGGCTGATTAACAGTCA 905
QY 302 sGluGlyTyRglyTyRserAspGlu 310
Db 906 TGAGGGGTATGATACAGCATGAA 930

RESULT 11
AAZ54613
ID AAZ54613 standard; DNA; 963 BP.
XX
AC AAZ54613;
XX
DT 21-MAR-2000 (first entry)

XX Neisseria meningitidis ORF 406 partial DNA sequence SEQ ID NO:3109.
DE
XX Neisseria meningitidis; Neisseria gonorrhoeae; antigen; vaccine;
KW antigenic; diagnosis; immunogenic; infection; meningitis; septicemia;
KW antibacterial; gene therapy; ds.
XX
OS Neisseria meningitidis.
XX
XX WO957280-A2.
XX
XX 11-NOV-1999.
XX
XX 30-APR-1999; 99WO-US009346.
XX
XX 01-MAY-1998; 98US-0083758P.
XX
XX 31-JUL-1998; 98US-0094869P.
XX
XX 02-SEP-1998; 98US-0098994P.
XX
XX 02-SEP-1998; 98US-0099062P.
XX
XX 09-OCT-1998; 98US-0103749P.
XX
XX 09-OCT-1998; 98US-0103794P.
XX
XX 09-OCT-1998; 98US-0103796P.
XX
XX 25-FEB-1999; 99US-0121528P.
XX
XX (CHIR) CHIRON CORP.
XX (GENO-) INST GENOMIC RES.
XX
XX Fraser C, Galeotti C, Grandi G, Hickey E, Maignani V, Mora M;
PI Petersen J, Pitzer M, Rappuoli R, Ratti G, Scalato E, Scarselli M;
PI Tettelin H, Venter JC;
XX
XX MPI: 2000-062150/05.
XX P-PSDB; AAY75811.
XX
XX Novel Neisserial polypeptides predicted to be useful antigens for
PT vaccines and diagnostics.
XX
XX Example 1; Page 108-109; 1453pp; English.
XX
XX AA253015 to AA254536, AA254577 to AA254615, and AAY74253 to AAY75941
CC represent novel Neisseria meningitidis and N. gonorrhoeae polynucleotides
CC and polypeptides. AA254537 to AA254576 and AA254616 to AA255473 represent
CC PCR primers used in the exemplification of the present invention. The
CC polypeptides, the polynucleotides, antibodies and compositions of the
CC invention can be used as vaccines, as diagnostic reagents, and as
CC immunogenic compositions. The polypeptides can be used in the manufacture
CC of medicaments for treating or preventing infection due to Neisserial
CC bacteria (e.g. meningitis and septicemia), to detect the presence of
CC Neisseria bacteria, or to raise antibodies. They may also be used to
CC screen for agonists or antagonists, which may themselves have use as
CC antibacterial agents. The polynucleotides of the invention may also be
CC used in gene therapy protocols
XX
XX
XX Sequence 963 BP; 284 A; 234 C; 217 G; 228 T; 0 U; 0 Other;
SQ
Alignment Scores:
Pred. No.: 1,466-202 Length: 963
Score: 207.00 Matches: 307
Percent Similarity: 99.35% Conservativity: 0
Best Local Similarity: 99.35% Mismatches: 1
Query Match: 64.69% Indels: 2
DB: 3 Gaps: 0
US-10-617-835-4 (1-320) x AA254613 (1-963)
QY 3 AAlaA-GLLeuLeuIleProIleLeuPheSerValPheIleLeuSerAlaCyseGlyThrLeu 22
DB 7 GCAAGCGCTGCTATACCTATTTCTTTTTCAGTTTATTATTCGCCCGCGGACACTG 66
QY 23 ThrGlyIleProSerHisGlyGlyGlyIleValArgPheAlaValGluGlnGluLeuValAla 42.
DB 67 ACAAGTATTCATCCATGCGAGGTAAACCTTTGCGGTGGAACAAGAACTGTGCGC 126

QY 43 AAlaSerAlaArgAlaAlaValIleValSerMetAspLeuGlnAlaLeuHisGlyValArgIleVal 62
DB 127 GCTTCTGCGAGAGCTGCGCTTAAAGACATGATTTTACAGCACTTACACGAGCAAAAGTT 186
QY 63 AAlaLeuValIleAlaThrMetGlyValSerGlySerGlySerLeuThrGlyGlyValArgTyr 82
DB 187 GCATTGTACATTGCCACATATGGGCGACCAAGGTTTACAGCATGTTTACAGGGGGTCCGTCAC 246
QY 83 SerIleAspAlaLeuIleArgGlyGlyValIleValSerProAlaValArgThrAspTyr 102
DB 247 TCCATTGATGACCTGATTCGTGGCCAAATACATTAACAGCCGTGCGGTCCGATCCATTAC 306
QY 103 ThrTyrProArgTyrGlyThrThrAlaGluThrThrSerGlyGlyLeuThrGlyLeuThr 122
DB 307 ACCATTCACGTTACGAAACCAACCGCTGAAACAAATCACGGCGTTGACAGGTTTAAACC 366
QY 123 ThrSerLeuSerThrLeuAsnAlaProAlaLeuSerArgThrGlnSerAspGlySerGly 142
DB 367 ACTTCTTATATCTACACTTAATGCCCTGACTCTCTCGACCCAAATCAGACGGTAGCGGA 426
QY 143 SerArg-SerSerLeuGlyLeuAsnIleGlyGlyMetGlyAspTyrArgAsnGluThrIle 162
DB 427 AGTAA-AAGCAGTCTGGGCTTAATATTTGGCGGATGGGGGATTTATCGAAATGAACCTT 485
QY 162 UThrThrAsnProArgAspThrAlaPheLeuSerHisLeuValGlnThrValPhePhe 182
DB 486 GAGCACTAACCCGCGAGACACTGCTTTCTTCCACTTGGTACAGACCGTATTTTCTCT 545
QY 182 UArgGlyIleAspValIleSerProAlaAsnAlaAspThrAspValPheIleAsnIleAs 202
DB 546 GCGCGGCAATAGACGTTGTTTCTCTGCGCAATCCGATACAGATGTTTATTAACATGCA 605
QY 202 PValPheGlyThrIleArgAsnArgThrGluMetHisLeuTyrAsnAlaGlnThrLeu 222
DB 606 CGTATTCGGAACGATACCAACGAAACCGAAATGCACTATCAATGCGGAACACTGAA 665
QY 222 SAlaGlnThrIleValGluGlyThrPheAlaValAspArgThrAsnIleValLeuLeu 242
DB 666 AGCCCAACAAACATGGAATATTTGCGAGTACACGAAACCAATTAATAATTTCTCATCA 725
QY 242 SProIleThrAsnAlaPheGluAlaIleTyrLeuGlnAsnTyrAlaLeuTyrMetGlyPyr 262
DB 726 ACCAABAAACCAATGCTTTGAAGCTGCTATTAAGAAATTCGCAATTCGATGCGGCGC 785
QY 262 GTrIleValSerIleGlyIleValProThrGluGlyLeuMetValAspPheSerAsp 282
DB 786 GTATTAAGTAAAGCAAAAGAAATTAACCGACGAAAGATTAATGTCGATTTCTCCGATAT 845
QY 282 eArgProIleGlyAsnHisThrGlyAsnSerAlaProSerValGluAlaAspAsnSerHis 302
DB 846 CCGACCAATACGCAATCATACGGGTAACTCCGCCCATTCGTAAGAGCTGATTAACAGTCA 905
QY 302 eGluGlyTyrGlyTyrSerAspGlu 310
DB 906 TGAGCGGATGATGATACAGCATGAA 930
RESULT 12
AAA81296
ID AAA81296 standard; DNA; 963 BP.
AC AAA81296;
DT 04-DEC-2000 (first entry)
DE N. meningitidis partial DNA sequence m406.seq SEQ ID NO:1034.
XX Neisseria meningitidis; Neisseria gonorrhoeae; genome; immunogenic;
KW antigen; vaccine; diagnosis; infection; antibacterial; identification;
KW Meningococcus B; Memb; ds.
XX Neisseria meningitidis.
OS
XX
XX WO200022430-A2.

XX 20-APR-2000.
PD
XX
PF 08-OCT-1999; 99WO-US023573.
XX
XX 09-OCT-1998; 98US-0103794P.
PR 30-APR-1999; 99US-0132068P.
XX
PA (CHIR) CHIRON CORP.
XX
XX
XX Fraser CM, Hickey E, Peterson J, Tettelin H, Venter JC,
PI Massignani V, Galdootti C, Mora M, Rattli G, Scarcella M, Scarlato V,
PI Rapunoli R, Pizzo M;
XX
XX WPI: 2000-118079/27.
DR P-PSDB; AAB25656.
DR
XX
XX Isolated nucleotide sequences of *Neisseria meningitidis* which can be used
PT in the diagnosis and treatment of *N. meningitidis* infection and other
PT *Neisseria* infections, for example, *N.gonorrhoea*.

The present invention describes methods of obtaining immunogenic proteins from *Neisseria* genomic sequences. AAA81453 to AAA8214 represent specifically claimed *Neisseria meningitidis* genomic DNA sequences; AAA81260 to AAA81303 and AAB25620 to AAB25663 represent *Neisseria* DNA sequences and their corresponding proteins; AAA81254 to AAA81259 and AAA81304 to AAA81321 represent PCR primers used in the isolation of *Neisseria meningitidis* DNA sequences; and AAA81322 to AAA81452 represent *Neisseria meningitidis* MenB polynucleotide ORF sequences, which are all used in the exemplification of the present invention. The nucleic acid sequences, protein sequences, and antibodies against them, can be used in the manufacture of a composition. The composition can be used as a medicament (or in the manufacture of a medicament) for treating, preventing or diagnosing infection due to *Neisseria* bacteria. For example, some of the identified proteins could be components of vaccines against *Meningococcus B*; against all serotypes; and/or against all pathogenic *Neisseria*. Identification of sequences from the bacterium will also facilitate production of biological probes, particularly organism-specific probes. Attempts to make efficacious *Meningococcus B* vaccines have failed mainly due to antigen tolerance. Multivalent vaccines have also been tried but none have successfully overcome antigenic variability. The provision of further, complete sequences may provide an opportunity to identify secreted or surface exposed proteins that may be presumed targets for the immune system and which are not antigenically variable or at least more conserved than other more variable regions

QY	63	AlaLeuYrTlIeAlaThMeGlyAspGlnGlySerGlySePleuThrGlyVGIYArGTYr	82
Db	187	GGATTGTACATTGCCATCTATGGGGCAACAGGTTCAGGAGTTTGAACAGGGGTCCTAC	246
QY	83	SerIleAspAlaLeuIleAArgGlyGlyYrIleAsnSerProAlaValArGThraAspTYr	102
Db	247	TCGATTGATGCACTGATTCTGTGGCGAATACATTAACAGCGCTGCGTACCGATTAC	306
QY	103	ThTYrProArGYrGlyUThrThraIaGluThrThrSerGlyGlyLeuThrGlyLeuThr	122
Db	307	ACCTATCCACGTTACGAAACCCGCTGAACATCAGGCGGTTTGAACAGTTTAACC	366
QY	123	ThrSerLeuSerThrLeuAsnAlaProAlaLeuSerArGThrGlnSerAspGlySerGly	142
Db	367	ACTCTTTTATCTACACTTAATGCCCTGCACTCTCCGACCCCATCAGACGGTAGCGGA	426
QY	143	SerArG-SerSerLeuGlyLeuAsnIleGlyGlyMeGlyAspTYrArGAsnGlyUThrIle	162
Db	427	AGTAA-AAGCACTCTCGGGCTTAAATATGGCCGGATGGGGGATTTTCGAAAGAAACCTT	485
QY	162	UThrThraAspProArGAspThraAlaPheLeuSerHisLeuValGlnThrValPhePheIe	182
Db	486	GACGACTAACCCGGCCGACACTGCTTTCTTCCACTTGGTACAGACCGTATTTTCTT	545
QY	182	uAArgGlyIleAspValValSerProAlaAsnAlaAspThraAspValPheIleAsnIleAs	202
Db	546	GCGCGGCAATAGACGTTGTTCTTCCTGCCAATCCGATACAGATGTGTTATTAACTACGA	605
QY	202	pValPheGlyThrIleArGAsnArGThrGluMetHisLeuYrAsnAlaGluThrLeuIy	222
Db	606	CGTATTCCGACGATACCAACCAACAGAACCGAAATGCACTTATCAATAGCCGAAACACTGAA	665
QY	222	sAlaGlnThrIySleuGlyUtyrPheAlaValAspArGThraAsnIlySlyLeuLeuIlely	242
Db	666	AGCCCAACAAACCTGGAATATTTCCGAGTAAACAGAACCAATTAATAAATTCCTCATCA	725
QY	242	sProlySerThraAsnAlaPheGluAlaAlaTyrllySgluAsnTYrAlaLeuTrpMeGlyYr	262
Db	726	ACCAAAAAACAATGGGTTTGAAGCTGCTATTAACAAAAATTAACGCAATGTGGATGGGGCC	785
QY	262	oTYrIySValSerIySgIyIleIyPProThrGlnGlyLeuMeCValAspPheSerAspI1	282
Db	786	GTATTAAGTAACCAAGGAATTAACCGACGGAAGATTAAAGTGTGATTTCTCCGATAT	845
QY	282	eArGProTYrGlyAsnHisThrGlyAsnSerAlaProSerValGluAlaAspAsnSerHis	302
Db	846	CCGACCAATACGGCATCTATACCGGTAACTCCGCCCATCCGTAGAAGCGTAAACAGTCA	905
QY	302	sGluGlyTYrGlyTYrSerAspGlu 310	
Db	906	TGAGGGGTATGGATACAGCGATGAA 930	
RESULT 13			
XX	AAF21581	standard; DNA; 963 BP.	
XX	AAF21581;		
XX	13-MAR-2001	(first entry)	
DE	N. meningitidis partial DNA sequence m406.seq	SEQ ID NO:74.	
XX	Neisseria meningitidis; Neisseria gonorrhoeae; immunogenic; vaccine;		
KW	diagnosis; antigen; detection; infection; gene therapy; antibacterial;		
XX	ds.		
XX	Neisseria meningitidis.		
XX	PN	WO200066791-A1.	
XX	PD	09-NOV-2000.	
PF	08-MAR-2000; 2000WO-US005928.		

XX 30-APR-1999; 99US-0132068P.
 PR 08-OCT-1999; 99MO-US023573.
 PR 28-FEB-2000; 2000GB-00004695.
 XX
 PA (CHIR) CHIRON CORP.
 PA (GENO-) INST GENOMIC RES.
 XX
 PI Piza M, Hickey E, Peterson J, Tettein H, Venter JC,
 PI Masignani V, Galeotti C, Mora M, Ratti G, Scarselli M, Scarlato V,
 PI Rappuoli R, Frazer CM, Grandi G;
 XX
 DR MPI: 2000-647603/62.
 DR P-PSDB: AAB58586.
 XX
 PT *Neisseria meningitidis* B full length genome sequence and open reading
 PT frames are used to detect, treat and prevent *Neisseria* infections.
 XX
 PS Example 1; Page 108; 692pp; English.
 XX
 CC The present invention describes the full length genome of *Neisseria*
 CC meningitidis B (NMB). The sequences in AAF21544 and AAF21607 to AAF21613
 CC represent fragments of the NMB genomic sequence, as the sequence was too
 CC long to go in a record on its own it was split into 8 sequences which
 CC overlap each other at the beginning and end of each sequence by 49980 bp
 CC (i.e. the last 49980 bp of AAF21544 is repeated at the beginning of
 CC AAF21607, the last 49980 bp of AAF21607 are repeated at the beginning of
 CC AAF21608, and so on). AAF21545 to AAF21588 encode the *Neisseria* proteins
 CC given in AAB58550 to AAB58593, and AAF21589 to AAF21606 represent PCR
 CC primers which are used in the exemplification of the present invention.
 CC The NMB genome and fragments from it have antibacterial activity, and can
 CC be used in vaccines and gene therapy. *Neisseria* nucleic acids, proteins
 CC and/or antibodies which binds to the proteins can be used in compositions
 CC for treating or preventing infection due to *Neisseria* bacteria or as a
 CC diagnostic reagent for detecting the presence of *Neisseria* bacteria or
 CC of antibodies raised to *Neisseria* bacteria. Computer, computer memory,
 CC computer storage medium or computer databases can be used in a search to
 CC identify open reading frames (ORFs) or coding sequences within the NMB
 CC genome. The DNA sequences provide further opportunities to find antigenic
 CC or immunogenic proteins which are more effective in vaccines than the
 CC outer membrane proteins currently used
 XX
 SO Sequence 963 BP; 284 A; 234 C; 217 G; 228 T; 0 U; 0 Other:
 XX
 Alignment Scores:
 Pred. No.: 1,466-202 Length: 963
 Score: 207.00 Matches: 307
 Percent Similarity: 99.35% Conservative: 0
 Best Local Similarity: 99.35% Mismatches: 1
 Query Match: 64.69% Indels: 2
 DB: Gaps: 0
 US-10-617-835-4 (1-320) x AAF21581 (1-963)
 QY 3 AAlaAGLeuLeuLeuProCileuPheSerValPheileLeuSerAlaCysGlyThrLeu 22
 DB 7 GCAAGCGCTGCTGATACCTTATTTTTCAGTTTATTTATTTATTCGCCCTCGCGGACACTG 66
 QY 23 ThrGlyIleProSerHisGlyGlyGlyGlySerPheAlaValGluGlnGluLeuValAla 42
 DB 67 ACAAGTATTTCCATCGCATCGCGAGAGTAACGCTTTCGCGTGAACAAGAACTTGCGCC 126
 QY 43 AlaSerAlaAlaGAlAlaValAlaValAspMetAlaPheLeuGlnAlaLeuHisGlyValGlyVal 62
 DB 127 GCTTCGCGAGAGCTGCGCTTAAAGACATGATTTACAGGCACTTACACGAGAAAGTT 186
 QY 63 AlaLeuTYrIleAlaThrMetGlyAspGlnGlySerGlySerLeuThGlyValGlyTYr 82
 DB 187 GCATTGTGATTCGCACTATGCGGACCAAGATTTCAGGAGTTTACACAGGAGGTGCTAC 246
 QY 83 SerIleAspAlaLeuIleArgGlyGlyIleuTYrIleAsnSerProAlaValArgThrAspTYr 102
 DB 247 TCCATTGATGCACTGATTCGTGGCAATATCATAAACAGCCCTCGTCCGATCCATTAC 306

QY 103 ThrTYrProArgTYrGluThrThrAlaGluThrThrSerGlyGlyLeuThrGlyLeuThr 122
 DB 307 ACTTATCCACGTTAGAAACCAACCGCTGTAACAAATACAGGGGTTTGACAGATTTAAC 366
 QY 123 ThrSerLeuSerThrLeuAsnAlaProAlaLeuSerArgTYrGlnSerAspGlySerGly 142
 DB 367 ACTTCTTATCTACACTTATATGCCCTTCACCTCTCCGACCCATCAGACGGTATGCGGA 426
 QY 143 SerArg-SerSerLeuGlyLeuAsnIleGlyGlyMetGlyAspTYrArgAsnGluThrLe 162
 DB 427 AGTAA-AAAGAGTCTGGGCTTAAATATGCGCGGATGCGGATTTACAAAGAAACCTT 485
 QY 162 UThrThrAspProAspArgThrAlaPheLeuSerIleuValGlnThrValPhePheLe 182
 DB 486 GACGACTAACCCGCGGACACTGCTCTTCTTCCACTTGATGACAGACGATTTTCTCT 545
 QY 182 UArgGlyIleAspValAlaSerProAlaAsnAlaAspThrAspValPheIleAsnIleAs 202
 DB 546 GCGCGGCAATAGACGTTGTTCTCTGCGCAATGCGATACAGATGTTTATTATACATGCA 605
 QY 202 PValPheGlyThrIleArgAsnArgThGluMetHisLeuTYrAsnAlaGluThrLeuLY 222
 DB 606 CGTATTCGGAACGATACCGCAACAGAACCGAAATGCACTATACAAATGCCGAAACACTGAA 665
 QY 222 AlaGlnThrIleuGluTYrPheAlaValAspArgThrAsnIleuValGlyLeuIleLY 242
 DB 666 AGCCCAACCAAACTGGAATATTTGCGAGTACAGAACCAATTAATAATTTCTATCANA 725
 QY 242 sProLYsThrAsnAlaPheGluAlaAlaTYrLYsGluAsnTYrAlaLeuTYrMetGlyTYr 262
 DB 726 ACCAATAAACCAATGCTTTGAAGCTGCGCTATTAATAAATAATGCAATGCGATGCGGGCC 785
 QY 262 CTYrLYsValSerLYsGlyIleLYsProThGluGlyLeuMetValAspPheSerAspI 282
 DB 786 GTATTAAGATTAAGCAAAAGAAATTAACCGACGAAAGATTAATGTCGATTTCTCCGATAT 845
 QY 282 eArgProTYrGlyAsnHisThrGlyAsnSerAlaProSerValGluAlaAspAsnSerHis 302
 DB 846 CCGACCAATACGGCAATATACGGGTAACTCGGCCCATTCGTAAGGCTGATTAACGTCA 905
 QY 302 sGluGlyTYrGlyTYrSerAspGlu 310
 DB 906 TGAAGCGTATGATACAGCATGAA 930
 RESULT 14
 AAB1473
 ID AAB1473 standard; DNA; 92934 BP.
 XX
 AC AAB1473;
 XX
 DT 04-DEC-2000 (first entry)
 XX
 DE N. meningitidis partial DNA sequence gnm_21 SEQ ID NO:21.
 XX
 KW *Neisseria meningitidis*; *Neisseria gonorrhoeae*; genome; immunogenic;
 KW antigen; vaccine; diagnosis; infection; antibacterial; identification;
 KW *Meningococcus B*; *MenB*; *de*.
 XX
 OS *Neisseria meningitidis*.
 XX
 PN WO200022430-A2.
 XX
 PD 20-APR-2000.
 XX
 PF 08-OCT-1999; 99MO-US023573.
 XX
 PR 09-OCT-1998; 98US-0103794P.
 PR 30-APR-1999; 99US-0132068P.
 XX
 PA (CHIR) CHIRON CORP.
 PA
 PI Frazer CM, Hickey E, Peterson J, Tettein H, Venter JC;

PI Masignani V, Galeotti C, Mora M, Ratti G, Scarselli M, Scarlato V,
PI Rappuoli R, Pizza M,
XX WPI, 2000-318079/27.
DR
XX Isolated nucleotide sequences of *Neisseria meningitidis* which can be used
PT in the diagnosis and treatment of *N. meningitidis* infection and other
PT *Neisseria* infections, for example, *N. gonorrhoea*.
XX
XX Claim 7; Page 471-498; 1760pp; English.

XX The present invention describes methods of obtaining immunogenic proteins
CC from *Neisseria* genomic sequences. AAA81453 to AAA82414 represent
CC specifically claimed *Neisseria meningitidis* genomic DNA sequences;
CC AAA81260 to AAA81303 and AAA825620 to AAA825663 represent *Neisseria* DNA
CC sequences and their corresponding proteins; AAA81254 to AAA81259 and
CC AAA81304 to AAA81321 represent PCR primers used in the isolation of
CC *Neisseria meningitidis* DNA sequences; and AAA81322 to AAA81452 represent
CC *Neisseria meningitidis* MemB polynucleotide ORF sequences, which are all
CC used in the exemplification of the present invention. The nucleic acid
CC sequences, protein sequences, and antibodies against them, can be used in
CC the manufacture of a composition. The composition can be used as a
CC medicament (or in the manufacture of a medicament) for treating,
CC preventing or diagnosing infection due to *Neisseria* bacteria. For
CC example, some of the identified proteins could be components of vaccines
CC against *Neisseria* B, against all serotypes; and/or against all
CC pathogenic *Neisseria*. Identification of sequences from the bacterium
CC will also facilitate production of biological probes, particularly
CC organism-specific probes. Attempts to make efficacious *Neisseria* B
CC vaccines have failed mainly due to antigen tolerance. Multivalent
CC vaccines have also been tried but none have successfully overcome
CC antigenic variability. The provision of further, complete sequences may
CC provide an opportunity to identify secreted or surface exposed proteins
CC that may be pressed targets for the immune system and which are not
CC antigenically variable or at least more conserved than other more
CC variable regions
XX
XX Sequence 92934 BP; 24051 A; 24249 C; 21902 G; 22730 T; 0 U; 2 Other;

Alignment Scores:

Pred. No.: 3.09e-187 Length: 92934
Score: 194.00 Matches: 307
Percent Similarity: 99.03% Conservative: 0
Best Local Similarity: 99.03% Mismatches: 1
Query Match: 60.62% Indels: 3
DB: Gaps: 0

US-10-617-835-4 (1-320) x AAA81473 (1-92934)

QY 3 AlAaTgLeuLeuLleProlleLeuPheSerValPheIleuSerAlaCYeGlyThrLeu 22
DB 18031 GCACGGCTGCGATACCATCTTTTTCAGTTTATTTATTCGCGCTGGGACACTG 18090
QY 23 ThGlylLePProSerHisGlyGlyLysArgPheAlaValGluGlnGluLeuValAla 42
DB 18091 ACAGGTATTCATCGCATGCGGAGGTAAAGCTTTGCGGTGCAACAAGACTTGCGCC 18150
QY 43 AlAaSerlAaArgAlaAlaValLysAspMetAspLeuGlnAlaLuhISGlyArgLysVal 62
DB 18151 GCTTCTGCAAGAGTGGCGTTAAAGACATGGAATTACAGGATTAACGAGCAAAAGTT 18210
QY 63 AlAaLeuTyrIleAlaThMetGlyAspGlnGlySerGlySerLeuThr-GlyGlyArgTy 82
DB 18211 GCATTGATCATTTGCCACATGGGCGACCAAGTTTCAGGCACTTTGACAGGGGGGTCCGTA 18270
QY 82 rSerIleAspAlaLeuLleArgGlyGlyTyrIleAsnSerProAlaValArgThrAspTy 102
DB 18271 CTCATGATGACATCGATTGCGTGGGAATACATTAACAGCCCTGCGTACGATTA 18330
QY 102 rThTyTProArgGlyGlyGluThrAlaGluThrThSerGlyGlyLeuThrGlyLeuTh 122
DB 18331 CACCTATCCACGTTACGAAACCAACCGCTGAAACAACATCAGCGGTTTGACAGGTTTAAC 18390

QY 122 rThSerLeuSerThrLeuAsnAlaProAlaLeuSerArgThrGlnSerAspGlySerGly 142
DB 18391 CACTTCTTTATCATCATTAATGCGCTGGACCTCTCGACCAATCAAGCGGTAGCGG 18450
QY 142 ySerArg-SerSerLeuGlyLeuAsnIleGlyGlyMetGlyAspTyArgAsnGluThrL 162
DB 18451 AAGTAA-AAGCAGCTCTGGGCTTAAATTTGGCGGGAATGAGGATTAACGAAATAACT 18509
QY 162 eUThrTrnAsnProArgAspThrAlaPheLeuSerHisLeuValGluThrValPhePheL 182
DB 18510 TGACGACTAACCCCGCGGACATGCTCTTTCTTCCACTTGGTACAGACCGATTTTTC 18569
QY 182 eUArgGlyIleAspValValSerProAlaAsnAlaAspThrAspValPheIleAsnIleA 202
DB 18570 TGCGCGCATAGACGTTGTTCTCTCGCATGCGCATGCGATGATGCTTTATTAACATCG 18629
QY 202 sPValPheGlyThrIleArgAsnArgThrGluMetHisLeuTyrAsnAlaGluThrLeuL 222
DB 18630 ACGTATTCGAAACCATGCGAACGAAATGCACTATACATGCGAAACACTGA 18689
QY 222 ySAlaGlnThrLysLeuGlyTyrPheAlaValAspArgThrAsnLysLeuLeuIleL 242
DB 18690 AAGCCAAACAAACCTGAATATTTCCAGTACAGACAAACATTAATGCTCATCA 18749
QY 242 ySPProLysThrAsnAlaPheGluAlaAlaTyrLysGluAsnTyrAlaLeuThrMetGlyP 262
DB 18750 AACCMAAACCAATGCGTTGAAGCTGCTATTAAGAAATTAAGCATGCGATGGGCGC 18809
QY 262 rOTyTyrLysValSerLysGlyIleLysProThrGluGlyLeuMetValAspPheSerAspI 282
DB 18810 CGTTAAAGTAAGCAAGAAAGAAATTAACCGACGAAAGATTAAGTGCATTTCTCCATA 18869
QY 282 lAaArgProTyrGlyAsnHisGThrGlyAsnSerAlaProSerValGluAlaAspAsnSerH 302
DB 18870 TCCGACCATACCGGACATCATACGGGTACTCCGCCCATCGTGAAGCTGATTAACGTC 18929
QY 302 lSgGlyTyrGlyTyrSerAspGlu 310
DB 18930 ATGAGGGGTATGATACAGCATGAA 18955

RESULT 15

AAA81489_7
Continuation (8 of 9) of AAA81489 from base 700001 (N. meningitidis partial DNA sequence
WP Sequence split into 9 fragments LOCUS AAA81489 Accession Aaa81489

WP	Fragment Name	Begin	End
WP	AAA81489_1	1	110000
WP	AAA81489_2	100001	210000
WP	AAA81489_3	200001	310000
WP	AAA81489_4	300001	410000
WP	AAA81489_5	400001	510000
WP	AAA81489_6	500001	610000
WP	AAA81489_7	600001	710000
WP	AAA81489_8	700001	810000
WP	AAA81489_9	800001	837096

Alignment Scores:

Pred. No.: 3.65e-187 Length: 110000
Score: 194.00 Matches: 307
Percent Similarity: 99.03% Conservative: 0
Best Local Similarity: 99.03% Mismatches: 1
Query Match: 60.62% Indels: 3
DB: Gaps: 0

US-10-617-835-4 (1-320) x AAA81489_7 (1-110000)

QY 3 AlAaTgLeuLeuLleProlleLeuPheSerValPheIleuSerAlaCYeGlyThrLeu 22
DB 86469 GCAAGGCTGCTGATCATCTATCTTTTTCAGTTTATTTATTCGCGCTGGGACACTG 86528
QY 23 ThGlylLePProSerHisGlyGlyLysArgPheAlaValGluGlnGluLeuValAla 42
DB 86529 ACAGGTATTCATCGCATGCGGAGGTAAAGCTTTGCGGTGCAACAAGACTTGCGCC 86588

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QY 43 A1aSerAlaArgAlaAlaValIleAspMetAspLeuGlnAlaLeuHisGlyValArgIleVal 62
DB |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
DB 86589 GCTTCTGCCAGAGCTGCCGTTAAAGACATGGATTACAGGCTTACACGACGAAAGTT 86648
QY 63 A1aLeuTyrIleAlaThrMetGlyAspGlnGlySerGlySerLeuThr-GlyGlyArgTyr 82
DB |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
DB 86649 GCATTGTACATTGCGCATATGGGCGCACCAAGTTCCAGGCACTTTGACAGGGGGGTGCTA 86708
QY 82 rSerIleAspAlaLeuIleArgGlyGlyTyrIleAsnSerProAlaValArgThrAspTyr 102
DB |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
DB 86709 CTCCATTGATGCACGATTCTGGGGAATACATAAACGCCCTGCCCTCCGTACCGATTAA 86768
QY 102 rThrTyrProArgTyrGlyTyrThrAlaGlyTyrThrSerGlyGlyLeuThrGlyLeuThr 122
DB |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
DB 86769 CACCTATCCAGCTTACGAAACCAACCGCTGAAACACATCAGGCGGTTGACAGGTTTAAAC 86828
QY 122 rThrSerLeuSerThrLeuAsnAlaProAlaLeuSerArgThrGlnSerAspGlySerGly 142
DB |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
DB 86829 CACTTCTTATCTACACTTAATGCCCTGCACTCTCTCGACCCCAATCAGACGGTAGCGG 86888
QY 142 ySerArg-SerSerLeuGlyLeuAsnIleGlyGlyMetGlyAspTyrArgAsnGlyTyrL 162
DB |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
DB 86889 AAGTAA-AAGCAGTCTGGCTTAAATATTTGGCGGATGGGATATATCGAAATGAACCT 86947
QY 162 eutThrThrAspProArgAspThrAlaPheLeuSerHisLeuValGlnThrValPhePheL 182
DB |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
DB 86948 TGACGACTTACCCCGGCGCACCTGCCCTTTCTTCCACTTGGTACAGACCGTATTTTTC 87007
QY 182 euArgGlyIleAspValIleSerProAlaAsnAlaAspThrAspValPheIleAsnIleA 202
DB |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
DB 87008 TGCGGGGATAGACGTTGTTCTCTCTGCCAATGCCGATACAGATGTGTTATTATACATCG 87067
QY 202 spValPheGlyThrIleArgAsnArgThrGlnMetHisLeuTyrAsnAlaGlyTyrLeuL 222
DB |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
DB 87068 ACGTATTCGGAACGATACGAAACGAAATGCACTTATACAAATGCCGAAACACTGA 87127
QY 222 ySalGlnThrIleGlnGlyTyrPheAlaValAspArgThrAsnIleAspLeuIleL 242
DB |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
DB 87128 AAGCCCAAAACAACTGGAATATTTCCAGTACGACGAAACCAATTAATAATTTGCTCATCA 87187
QY 242 ySProLySThrAsnAlaPheGlnAlaAlaTyrIleGlyAsnTyrAlaLeuTyrMetGlyP 262
DB |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
DB 87188 AACCAAAAACCAATGCGTTTGAAGCTGCTATTAAGAAATTAACGATGTGATGGGGC 87247
QY 262 rGlyTyrValSerIleGlyIleIleYSPThrGlnGlyLeuMetValAspPheSerAspI 282
DB |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
DB 87248 CGTATTAAGTAAGCAAAAGAAATTAAACGACGAAAGATTAATGCTCGATTCTCCGATA 87307
QY 282 leAspProTyrGlyAsnHisThrGlyAsnSerAlaProSerValGlnAlaAspAsnSerH 302
DB |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
DB 87308 TCCGACCATACGCGCATATATCGGGTAACTCCGCCCATCCGTAGAGGCTGATTAACAGTC 87367
QY 302 IsGlnGlyTyrGlyTyrSerAspGlu 310
DB |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
DB 87368 ATGAGGGGTATGATACAGCATGAA 87393
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Search completed: August 19, 2005, 03:34:00
Job time : 605 secs

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